

SEQUENCE LISTING

5 <110> SunGene GmbH Co. KGaA

<120> Method for the production of Astaxanthin in flowers of plants

10 <130> PF 53862

15 <160> 172

20 <170> PatentIn version 3.1

25 <210> 1

<211> 1771

<212> DNA

30 <213> Haematococcus pluvialis

35 <220>

<221> CDS

<222> (166)..(1155)

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	105 110 115	
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Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp

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Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp
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Thr Lys Gly Ile Thr Met Ala Leu Arg Val Ile Gly Ser Trp Ala Ala
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Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp
 85 90 95

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Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser
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Gly Thr Ser Ser Leu Leu Asp Ile Val Val Val Phe Phe Val Leu Glu
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Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly
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Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val
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Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys
 165 170 175

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His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp
 180 185 190

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Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met
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Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr
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Val Val, Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe
 225 230 235 240

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Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly
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Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser
 260 265 270

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Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp
 275 280 285

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Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His
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 Ala Ser Ala Leu Met Val Glu Gln Lys Gly Ser Glu Ala Ala Ala Ser
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20 agc cca gac gtc ttg aga gcg tgg gcg aca cag tat cac atg cca tcc 272
 Ser Pro Asp Val Leu Arg Ala Trp Ala Thr Gln Tyr His Met Pro Ser
 20 25 30 35

25 gag tcg tca gac gca gct cgt cct gcg cta aag cac gcc tac aaa cct 320
 Glu Ser Ser Asp Ala Ala Arg Pro Ala Leu Lys His Ala Tyr Lys Pro
 40 45 50

30 cca gca tct gac gcc aag ggc atc acg atg gcg ctg acc atc att ggc 368
 Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr Ile Ile Gly
 55 60 65

35 acc tgg acc gca gtg ttt tta cac gca ata ttt caa atc agg cta ccg 416
 Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile Arg Leu Pro
 70 75 80

40 aca tcc atg gac cag ctt cac tgg ttg cct gtg tcc gaa gcc aca gcc 464
 Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu Ala Thr Ala
 85 90 95

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 Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala Ala Val Phe
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 Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp
 120 125 130

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	Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Ser Met	
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	aaa gac cct gac ttc cac aag gga aat ccc ggc ctt gtc ccc tgg ttc	752
	Lys Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val Pro Trp Phe	
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	Ala Trp Trp Ala Val Val Met Gln Met Leu Gly Ala Pro Met Ala Asn	
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25	ctc cta gtc ttc atg gct gca gcc cca atc ttg tca gca ttc cgc ctc	896
	Leu Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu	
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30	Phe Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro Gly Pro Ala	
	245 250 255	
	gca ggc tct cag gtg atg gcc tgg ttc agg gcc aag aca agt gag gca	992
	Ala Gly Ser Gln Val Met Ala Trp Phe Arg Ala Lys Thr Ser Glu Ala	
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	tct gat gtg atg agt ttc ctg aca tgc tac cac ttt gac ctg cac tgg	1040
	Ser Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp	
	280 285 290	
40	gag cac cac agg tgg ccc ttt gcc ccc tgg tgg cag ctg ccc cac tgc	1088
	Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu Pro His Cys	
	295 300 305	
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 310 315 320

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 35 40 45

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Tyr Lys Pro Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr
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 Ile Ile Gly Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile
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10 Arg Leu Pro Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu
 85 90 95

15 Ala Thr Ala Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala
 100 105 110

20 Ala Val Phe Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr
 115 120 125

Thr His Asp Ala Met His Gly Thr Ile Ala Leu Arg His Arg Gln Leu
 130 135 140

25 Asn Asp Leu Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp
 145 150 155 160

30 Tyr Ser Met Leu His Arg Lys His Trp Glu His His Asn His Thr Gly
 165 170 175

35 Glu Val Gly Lys Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val
 180 185 190

40 Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe
 195 200 205

Ala Arg Leu Ala Trp Trp Ala Val Val Met Gln Met Leu Gly Ala Pro
 210 215 220

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11

Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala
 225 230 235 240

5 Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro
 245 250 255

10 Gly Pro Ala Ala Gly Ser Gln Val Met Ala Trp Phe Arg Ala Lys Thr
 260 265 270

15 Ser Glu Ala Ser Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp
 275 280 285

Leu His Trp Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu
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<213> Agrobacterium aurantiacum

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<222> (1)..(729)

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10	gcg ctg tgg ttt ctg gac gca gcg gcg cat ccc atc ctg gcg atc gca	144
	Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala	
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15	aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg	192
	Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala	
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	Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp	
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30	cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc	336
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	100 105 110	
35	gac gac gac ccc gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc	384
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	115 120 125	
40	cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc	432
	Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro	
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45	gtc atc gtg acg gtc tat gcg ctg atc ctt ggg gat cgc tgg atg tac	480
	Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr	
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50	gtg gtc ttc tgg ccg ctg ccg tcg atc ctg gcg tcg atc cag ctg ttc	528
	Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe	
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55	gtg ttc ggc acc tgg ctg ccg cac cgc ccc ggc cac gac gcg ttc ccg	576

13

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	Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala	
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5	His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn				
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					80
10	Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp				
		85		90	95
	Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr				
		100		105	110
15	Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala				
		115		120	125
20	Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro				
		130		135	140
25	Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr				
		145		150	155
					160
30	Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe				
		165		170	175
	Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro				
		180		185	190
35	Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu				
		195		200	205
40	Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His				
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Thr Ala

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<210> 7

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<212> DNA

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Gly Thr Thr Gly Asp Thr Ile Val Asn Leu Gly Leu Thr Ala Ala Ile

10

15

20

ctg ctg tgc tgg ctg gtc ctg cac gcc ttt acg cta tgg ttg cta gat 212

Leu Leu Cys Trp Leu Val Leu His Ala Phe Thr Leu Trp Leu Leu Asp

40

25

30

35

gcg gcc gcg cat ccg ctg ctt gcc gtg ctg tgc ctg gct ggg ctg acc 260

Ala Ala Ala His Pro Leu Leu Ala Val Leu Cys Leu Ala Gly Leu Thr

40

45

50

45

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5	tcc gtg gtg ccg ggg cgg ccg cgc gcc aat gcg gcg atc ggg caa ctg	356
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10	gcg ctg tgg ctc tat gcg ggg ttc tgg tgg ccc aag ctg atc gcc aag	404
	Ala Leu Trp Leu Tyr Ala Gly Phe Ser Trp Pro Lys Leu Ile Ala Lys	
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	105 110 115	
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	Gly His Gly Gly Pro Val Arg Trp Tyr Gly Ser Phe Val Ser Thr Tyr	
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	Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr Val Ile Phe Trp Pro Val	
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	Pro His Arg Pro Gly His Asp Asp Phe Pro Asp Arg His Asn Ala Arg	
	185 190 195	
45	tgg acc ggc atc ggc gac ccg ttg tca cta ctg acc tgc ttc cat ttc	740
	Ser Thr Gly Ile Gly Asp Pro Leu Ser Leu Leu Thr Cys Phe His Phe	
	200 205 210	
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	Gly Gly Tyr His His Glu His His Leu His Pro His Val Pro Trp Trp	
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 235 240

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<213> *Alcaligenes* sp.

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15	Cys Leu Ala Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala 50 55 60		
20	His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn 65 70 75 80		
25	Ala Ala Ile Gly Gln Leu Ala Leu Trp Leu Tyr Ala Gly Phe Ser Trp 85 90 95		
30	Pro Lys Leu Ile Ala Lys His Met Thr His His Arg His Ala Gly Thr 100 105 110		
35	Asp Asn Asp Pro Asp Phe Gly His Gly Gly Pro Val Arg Trp Tyr Gly 115 120 125		
40	Ser Phe Val Ser Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro 130 135 140		
45	Val Ile Val Thr Thr Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr 145 150 155 160		
	Val Ile Phe Trp Pro Val Pro Ala Val Leu Ala Ser Ile Gln Ile Phe 165 170 175		
	Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Asp Phe Pro 180 185 190		

Asp Arg His Asn Ala Arg Ser Thr Gly Ile Gly Asp Pro Leu Ser Leu
 195 200 205
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Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
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 225 230 235 240

15 Arg Ala

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 45 Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His

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	Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Val Ala			
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	aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg	192		
	Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala			
	50	55	60	
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	cat gac gcg atg cac ggg tcg gtc gtg cgg ggg cgt ccg cgc gcc aat	240		
	His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn			
	65	70	75	80
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	gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg	288		
	Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp			
	85	90	95	
	cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc	336		
20	Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr			
	100	105	110	
	gac gac gac cca gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc	384		
	Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala			
25	115	120	125	
	cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc	432		
	Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro			
	130	135	140	
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	145	150	155	160
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	Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe			
	165	170	175	
	gtg ttc ggc act tgg ctg ccg cac cgc ccc ggc cac gac gcg ttc ccg	576		
40	Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro			
	180	185	190	
	gac cgc cat aat gcg cgg tcg tcg cgg atc agc gac cct gtg tcg ctg	624		
	Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu			
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 Thr Ala

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 20 <213> Paracoccus marcusii

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 35 40 45

40 Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
 50 55 60

45 His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
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Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
85 90 95

5 Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
100 105 110

10 Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
115 120 125

15 Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
130 135 140

20 Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
145 150 155 160

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
165 170 175

25 Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
180 185 190

30 Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
195 200 205

35 Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
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Thr Ala

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 25 gtc tgt gca gcc tat ttg ctc caa cgg ggc ttg ggg gtg acg tta cta 96
 Val Cys Ala Ala Tyr Leu Leu Gln Arg Gly Leu Gly Val Thr Leu Leu
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 30 gaa aag cgg gaa gta cca ggg ggg gcg gcc acc aca gaa gct ctc atg 144
 Glu Lys Arg Glu Val Pro Gly Gly Ala Ala Thr Thr Glu Ala Leu Met
 35 40 45
 ccg gag cta tcc ccc cag ttt cgc ttt aac cgc tgt gcc att gac cac 192
 35 Pro Glu Leu Ser Pro Gln Phe Arg Phe Asn Arg Cys Ala Ile Asp His
 50 55 60
 gaa ttt atc ttt ctg ggg ccg gtg ttg cag gag cta aat tta gcc cag 240
 Glu Phe Ile Phe Leu Gly Pro Val Leu Gln Glu Leu Asn Leu Ala Gln
 40 65 70 75 80
 tat ggt ttg gaa tat tta ttt tgt gac ccc agt gtt ttt tgt ccg ggg 288
 Tyr Gly Leu Glu Tyr Leu Phe Cys Asp Pro Ser Val Phe Cys Pro Gly
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24

	ctg gat ggc caa gct ttt atg agc tac cgt tcc cta gaa aaa acc tgt	336
	'Leu Asp Gly Gln Ala Phe Met Ser Tyr Arg Ser Leu Glu Lys Thr Cys	
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5	gcc cac att gcc acc tat agc ccc cga gat gcg gaa aaa tat cgg caa	384
	Ala His Ile Ala Thr Tyr Ser Pro Arg Asp Ala Glu Lys Tyr Arg Gln	
	115 120 125	
10	ttt gtc aat tat tgg acg gat ttg ctc aac gct gtc cag cct gct ttt	432
	Phe Val Asn Tyr Trp Thr Asp Leu Leu Asn Ala Val Gln Pro Ala Phe	
	130 135 140	
15	aat gct ccg ccc cag gct tta cta gat tta gcc ctg aac tat ggt tgg	480
	Asn Ala Pro Pro Gln Ala Leu Leu Asp Leu Ala Leu Asn Tyr Gly Trp	
	145 150 155 160	
20	gaa aac tta aaa tcc gtg ctg gcg atc gcc ggg tcg aaa acc aag gcg	528
	Glu Asn Leu Lys Ser Val Leu Ala Ile Ala Gly Ser Lys Thr Lys Ala	
	165 170 175	
	ttg gat ttt atc cgc act atg atc ggc tcc ccg gaa gat gtg ctc aat	576
	Leu Asp Phe Ile Arg Thr Met Ile Gly Ser Pro Glu Asp Val Leu Asn	
	180 185 190	
25	gaa tgg ttc gac agc gaa cgg gtt aaa gct cct tta gct aga cta tgt	624
	Glu Trp Phe Asp Ser Glu Arg Val Lys Ala Pro Leu Ala Arg Leu Cys	
	195 200 205	
30	tcg gaa att ggc gct ccc cca tcc caa aag ggt agt agc tcc ggc atg	672
	Ser Glu Ile Gly Ala Pro Pro Ser Gln Lys Gly Ser Ser Ser Gly Met	
	210 215 220	
35	atg atg gtg gcc atg cgg cat ttg gag gga att gcc aga cca aaa gga	720
	Met Met Val Ala Met Arg His Leu Glu Gly Ile Ala Arg Pro Lys Gly	
	225 230 235 240	
40	ggc act gga gcc ctc aca gaa gcc ttg gtg aag tta gtg caa gcc caa	768
	Gly Thr Gly Ala Leu Thr Glu Ala Leu Val Lys Leu Val Gln Ala Gln	
	245 250 255	
	ggg gga aaa atc ctc act gac caa acc gtc aaa cgg gta ttg gtg gaa	816
	Gly Gly Lys Ile Leu Thr Asp Gln Thr Val Lys Arg Val Leu Val Glu	
	260 265 270	
45	aac aac cag gcg atc ggg gtg gag gta gct aac gga gaa cag tac cgg	864

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	Ala	Lys	Lys	Gly	Val	Ile	Ser	Asn	Ile	Asp	Ala	Arg	Arg	Leu	Phe	Leu	
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10	caa	ttg	gtg	gaa	ccg	ggg	gcc	cta	gcc	aag	gtg	aat	caa	aac	cta	ggg	960
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	305					310				315					320		
15	gaa	cga	ctg	gaa	cgg	cgc	act	gtg	aac	aat	aac	gaa	gcc	att	tta	aaa	1008
	Glu	Arg	Leu	Glu	Arg	Arg	Thr	Val	Asn	Asn	Asn	Glu	Ala	Ile	Leu	Lys	
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20	atc	gat	tgt	gcc	ctc	tcc	ggg	tta	ccc	cac	ttc	act	gcc	atg	gcc	ggg	1056
	Ile	Asp	Cys	Ala	Leu	Ser	Gly	Leu	Pro	His	Phe	Thr	Ala	Met	Ala	Gly	
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25	ccg	gag	gat	cta	acg	gga	act	att	ttg	att	gcc	gac	tcg	gta	cgc	cat	1104
	Pro	Glu	Asp	Leu	Thr	Gly	Thr	Ile	Leu	Ile	Ala	Asp	Ser	Val	Arg	His	
		355					360					365					
30	gtc	gag	gaa	gcc	cac	gcc	ctc	att	gcc	ttg	ggg	caa	att	ccc	gat	gct	1152
	Val	Glu	Glu	Ala	His	Ala	Leu	Ile	Ala	Leu	Gly	Gln	Ile	Pro	Asp	Ala	
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	Asn	Pro	Ser	Leu	Tyr	Leu	Asp	Ile	Pro	Thr	Val	Leu	Asp	Pro	Thr	Met	
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	Ala	Pro	Pro	Gly	Gln	His	Thr	Leu	Trp	Ile	Glu	Phe	Phe	Ala	Pro	Tyr	
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45	cgc	atc	gcc	ggg	ttg	gaa	ggg	aca	ggg	tta	atg	ggc	aca	ggg	tgg	acc	1296
	Arg	Ile	Ala	Gly	Leu	Glu	Gly	Thr	Gly	Leu	Met	Gly	Thr	Gly	Trp	Thr	
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50	gat	gag	tta	aag	gaa	aaa	gtg	gcg	gat	cgg	gtg	att	gat	aaa	tta	acg	1344
	Asp	Glu	Leu	Lys	Glu	Lys	Val	Ala	Asp	Arg	Val	Ile	Asp	Lys	Leu	Thr	
		435					440					445					
55	gac	tat	gcc	cct	aac	cta	aaa	tct	ctg	atc	att	ggg	cgc	cga	gtg	gaa	1392
	Asp	Tyr	Ala	Pro	Asn	Leu	Lys	Ser	Leu	Ile	Ile	Gly	Arg	Arg	Val	Glu	

	450	455	460	
	agt ccc gcc gaa ctg gcc caa cgg ctg gga agt tac aac ggc aat gtc			1440
	Ser Pro Ala Glu Leu Ala Gln Arg Leu Gly Ser Tyr Asn Gly Asn Val			
5	465	470	475	480
	tat cat ctg gat atg agt ttg gac caa atg atg ttc ctc cgg cct cta			1488
	Tyr His Leu Asp Met Ser Leu Asp Gln Met Met Phe Leu Arg Pro Leu			
		485	490	495
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	ccg gaa att gcc aac tac caa acc ccc atc aaa aat ctt tac tta aca			1536
	Pro Glu Ile Ala Asn Tyr Gln Thr Pro Ile Lys Asn Leu Tyr Leu Thr			
		500	505	510
15				
	ggg gcg ggt acc cat ccc ggt ggc tcc ata tca ggt atg ccc ggt aga			1584
	Gly Ala Gly Thr His Pro Gly Gly Ser Ile Ser Gly Met Pro Gly Arg			
		515	520	525
	aat tgc gct cgg gtc ttt tta aaa caa caa cgt cgt ttt tgg taa			1629
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		20	25	30
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	Glu Lys Arg Glu Val Pro Gly Gly Ala Ala Thr Thr Glu Ala Leu Met			
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Pro Glu Leu Ser Pro Gln Phe Arg Phe Asn Arg Cys Ala Ile Asp His
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Glu Phe Ile Phe Leu Gly Pro Val Leu Gln Glu Leu Asn Leu Ala Gln
 65 70 75 80

10

Tyr Gly Leu Glu Tyr Leu Phe Cys Asp Pro Ser Val Phe Cys Pro Gly
 85 90 95

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Leu Asp Gly Gln Ala Phe Met Ser Tyr Arg Ser Leu Glu Lys Thr Cys
 100 105 110

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Ala His Ile Ala Thr Tyr Ser Pro Arg Asp Ala Glu Lys Tyr Arg Gln
 115 120 125

Phe Val Asn Tyr Trp Thr Asp Leu Leu Asn Ala Val Gln Pro Ala Phe
 130 135 140

25

Asn Ala Pro Pro Gln Ala Leu Leu Asp Leu Ala Leu Asn Tyr Gly Trp
 145 150 155 160

30

Glu Asn Leu Lys Ser Val Leu Ala Ile Ala Gly Ser Lys Thr Lys Ala
 165 170 175

35

Leu Asp Phe Ile Arg Thr Met Ile Gly Ser Pro Glu Asp Val Leu Asn
 180 185 190

40

Glu Trp Phe Asp Ser Glu Arg Val Lys Ala Pro Leu Ala Arg Leu Cys
 195 200 205

Ser Glu Ile Gly Ala Pro Pro Ser Gln Lys Gly Ser Ser Ser Gly Met
 210 215 220
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'Met Met, Val Ala Met Arg His Leu Glu Gly Ile Ala Arg Pro Lys Gly
 225 230 235 240

5 Gly Thr Gly Ala Leu Thr Glu Ala Leu Val Lys Leu Val Gln Ala Gln
 245 250 255

10 Gly Gly Lys Ile Leu Thr Asp Gln Thr Val Lys Arg Val Leu Val Glu
 260 265 270

15 Asn Asn Gln Ala Ile Gly Val Glu Val Ala Asn Gly Glu Gln Tyr Arg
 275 280 285

20 Ala Lys Lys Gly Val Ile Ser Asn Ile Asp Ala Arg Arg Leu Phe Leu
 290 295 300

Gln Leu Val Glu Pro Gly Ala Leu Ala Lys Val Asn Gln Asn Leu Gly
 305 310 315 320

25 Glu Arg Leu Glu Arg Arg Thr Val Asn Asn Asn Glu Ala Ile Leu Lys
 325 330 335

30 Ile Asp Cys Ala Leu Ser Gly Leu Pro His Phe Thr Ala Met Ala Gly
 340 345 350

35 Pro Glu Asp Leu Thr Gly Thr Ile Leu Ile Ala Asp Ser Val Arg His
 355 360 365

40 Val Glu Glu Ala His Ala Leu Ile Ala Leu Gly Gln Ile Pro Asp Ala
 370 375 380

Asn Pro Ser Leu Tyr Leu Asp Ile Pro Thr Val Leu Asp Pro Thr Met
 385 390 395 400

45

Ala Pro Pro Gly Gln His Thr Leu Trp Ile Glu Phe Phe Ala Pro Tyr
 405 410 415

5 Arg Ile Ala Gly Leu Glu Gly Thr Gly Leu Met Gly Thr Gly Trp Thr
 420 425 430

10 Asp Glu Leu Lys Glu Lys Val Ala Asp Arg Val Ile Asp Lys Leu Thr
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15 Asp Tyr Ala Pro Asn Leu Lys Ser Leu Ile Ile Gly Arg Arg Val Glu
 450 455 460

20 Ser Pro Ala Glu Leu Ala Gln Arg Leu Gly Ser Tyr Asn Gly Asn Val
 465 470 475 480

Tyr His Leu Asp Met Ser Leu Asp Gln Met Met Phe Leu Arg Pro Leu
 485 490 495

25 Pro Glu Ile Ala Asn Tyr Gln Thr Pro Ile Lys Asn Leu Tyr Leu Thr
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 20 25 30

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 Ile Ala Ala Trp Leu Val Leu His Val Gly Leu Met Phe Phe Trp Pro
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ctg acc ctt cac agc ctg ctg ccg gct ttg cct ctg gtg gtg ctg cag 192
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 50 55 60

30 acc tgg ctc tat gta ggc ctg ttc atc atc gcg cat gac tgc atg cac 240
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 65 70 75 80

35 ggc tcg ctg gtg ccg ttc aag ccg cag gtc aac cgc cgt atc gga cag 288
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 85 90 95

40 ctc tgc ctg ttc ctc tat gcc ggg ttc tcc ttc gac gct ctc aat gtc 336
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45 gag cac cac aag cat cac cgc cat ccc ggc acg gcc gag gat ccc gat 384
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	Phe Asp Glu Val Pro Pro His Gly Phe Trp His Trp Phe Ala Ser Phe	
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5	ttc ctg cac tat ttc ggc tgg aag cag gtc gcg atc atc gca gcc gtc	480
	Phe Leu His Tyr Phe Gly Trp Lys Gln Val Ala Ile Ile Ala Ala Val	
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10	Ser Leu Val Tyr Gln Leu Val Phe Ala Val Pro Leu Gln Asn Ile Leu	
	165 170 175	
	ctg ttc tgg gcg ctg ccc ggg ctg ctg tcg gcg ctg cag ctg ttc acc	576
	Leu Phe Trp Ala Leu Pro Gly Leu Leu Ser Ala Leu Gln Leu Phe Thr	
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	ttc ggc acc tat ctg ccg cac aag ccg gcc acg cag ccg ttc gcc gat	624
	Phe Gly Thr Tyr Leu Pro His Lys Pro Ala Thr Gln Pro Phe Ala Asp	
	195 200 205	
20	cgc cac aac gcg cgg acg agc gaa ttt ccc gcg tgg ctg tcg ctg ctg	672
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25	acc tgc ttc cac ttc ggc ttt cat cac gag cat cat ctg cat ccc gat	720
	Thr Cys Phe His Phe Gly Phe His His Glu His His Leu His Pro Asp	
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 35 40 45

20 Leu Thr Leu His Ser Leu Leu Pro Ala Leu Pro Leu Val Val Leu Gln
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Thr Trp Leu Tyr Val Gly Leu Phe Ile Ile Ala His Asp Cys Met His
 65 70 75 80

25 Gly Ser Leu Val Pro Phe Lys Pro Gln Val Asn Arg Arg Ile Gly Gln
 85 90 95

30 Leu Cys Leu Phe Leu Tyr Ala Gly Phe Ser Phe Asp Ala Leu Asn Val
 100 105 110

35 Glu His His Lys His His Arg His Pro Gly Thr Ala Glu Asp Pro Asp
 115 120 125

Phe Asp Glu Val Pro Pro His Gly Phe Trp His Trp Phe Ala Ser Phe
 130 135 140

40 Phe Leu His Tyr Phe Gly Trp Lys Gln Val Ala Ile Ile Ala Ala Val
 145 150 155 160

45 Ser Leu Val Tyr Gln Leu Val Phe Ala Val Pro Leu Gln Asn Ile Leu

165

170

175

5 Leu Phe Trp Ala Leu Pro Gly Leu Leu Ser Ala Leu Gln Leu Phe Thr
180 185 190

10 Phe Gly Thr Tyr Leu Pro His Lys Pro Ala Thr Gln Pro Phe Ala Asp
195 200 205

15 Arg His Asn Ala Arg Thr Ser Glu Phe Pro Ala Trp Leu Ser Leu Leu
210 215 220

20 Thr Cys Phe His Phe Gly Phe His His Glu His His Leu His Pro Asp
225 230 235 240

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35 <211> 777

<212> DNA

40 <213> Nostoc sp.

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<222> (1)..(777)

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 Ile Ala Cys Phe Ile Leu Phe Leu Trp Ala Ile Ser Leu Ile Leu Leu
 35 40 45
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 ctc tca ata gat aca tcc ata att cat aag agc tta tta ggt ata gcc 192
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 50 55 60
 20 atg ctt tgg cag acc ttc tta tat aca ggt tta ttt att act gct cat 240
 Met Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
 65 70 75 80
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 25 Asp Ala Met His Gly Val Val Tyr Pro Lys Asn Pro Arg Ile Asn Asn
 85 90 95
 ttt ata ggt aag ctc act cta atc ttg tat gga cta ctc cct tat aaa 336
 Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys
 30 100 105 110
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 Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp
 115 120 125
 35
 tta gac cct gat tat tac aat ggt cat ccc caa aac ttc ttt ctt tgg 432
 Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp
 130 135 140
 tat cta cat ttt atg aag tct tat tgg cga tgg acg caa att ttc gga 480
 40 Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly
 145 150 155 160
 tta gtg atg att ttt cat gga ctt aaa aat ctg gtg cat ata cca gaa 528
 45 Leu Val Met Ile Phe His Gly Leu Lys Asn Leu Val His Ile Pro Glu

PF :

35

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	caa cta ttt tat ttt ggt aca ttt ttg cct cat aaa aag cta gaa ggt Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly			624
	195	200	205	
10	ggt tat act aac ccc cat tgt gcg cgc agt atc cca tta cct ctt ttt Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe			672
	210	215	220	
15	tgg tct ttt gtt act tgt tat cac ttc ggc tac cac aag gaa cat cac Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His			720
	225	230	235	240
	gaa tac cct caa ctt cct tgg tgg aaa tta cct gaa gct cac aaa ata Glu Tyr Pro Gln Leu Pro Trp Trp Lys Leu Pro Glu Ala His Lys Ile			768
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	tct tta taa Ser Leu			777
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Ile Ala Cys Phe Ile Leu Phe Leu Trp Ala Ile Ser Leu Ile Leu Leu
 35 40 45
 5
 Leu Ser Ile Asp Thr Ser Ile Ile His Lys Ser Leu Leu Gly Ile Ala
 50 55 60
 10
 Met Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
 65 70 75 80
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 Asp Ala Met His Gly Val Val Tyr Pro Lys Asn Pro Arg Ile Asn Asn
 85 90 95
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 Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys
 100 105 110
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 Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp
 115 120 125
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 Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp
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 Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly
 145 150 155 160
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 Leu Val Met Ile Phe His Gly Leu Lys Asn Leu Val His Ile Pro Glu
 165 170 175
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 Asn Asn Leu Ile Ile Phe Trp Met Ile Pro Ser Ile Leu Ser Ser Val
 180 185 190
 Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly
 195 200 205

Gly Tyr, Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe
 210 215 220

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Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His
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ggc cca cct cct cat ctc cat cgg tca ttt gct gct acc acg atg ctg 95
 Gly Pro Pro Pro His Leu His Arg Ser Phe Ala Ala Thr Thr Met Leu
 45 20 25 30

	tcg aag ctg cag tca atc agc gtc aag gcc cgc cgc gtt gaa cta gcc	143
	Ser Lys Leu Gln Ser Ile Ser Val Lys Ala Arg Arg Val Glu Leu Ala	
	35 40 45	
5	cgc gac atc acg cgg ccc aaa gtc tgc ctg cat gct cag cgg tgc t'cg	191
	Arg Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser	
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10	tta gtt cgg ctg cga gtg gca gca cca cag aca gag gag gcg ctg gga	239
	Leu Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly	
	65 70 75	
	acc gtg cag gct gcc ggc gcg ggc gat gag cac agc gcc gat gta gca	287
15	Thr Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala	
	80 85 90 95	
	ctc cag cag ctt gac cgg gct atc gca gag cgt cgt gcc cgg cgc aaa	335
20	Leu Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys	
	100 105 110	
	cgg gag cag ctg tca tac cag gct gcc gcc att gca gca tca att ggc	383
	Arg Glu Gln Leu Ser Tyr Gln Ala Ala Ala Ile Ala Ala Ser Ile Gly	
	115 120 125	
25	gtg tca ggc att gcc atc ttc gcc acc tac ctg aga ttt gcc atg cac	431
	Val Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His	
	130 135 140	
30	atg acc gtg ggc ggc gca gtg cca tgg ggt gaa gtg gct ggc act ctc	479
	Met Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu	
	145 150 155	
	ctc ttg gtg gtt ggt ggc gcg ctc ggc atg gag atg tat gcc cgc tat	527
35	Leu Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr	
	160 165 170 175	
	gca cac aaa gcc atc tgg cat gag tgc cct ctg ggc tgg ctg ctg cac	575
40	Ala His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His	
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	Lys Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu	
	195 200 205	
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39

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	Phe Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu	
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10	ggc atc acg cta tac ggc atg gca tat atg ttt gta cac gat ggc ctg	767
	Gly Ile Thr Leu Tyr Gly Met Ala Tyr Met Phe Val His Asp Gly Leu	
	240 245 250 255	
15	gtg cac agg cgc ttt ccc acc ggg ccc atc gct ggc ctg ccc tac atg	815
	Val His Arg Arg Phe Pro Thr Gly Pro Ile Ala Gly Leu Pro Tyr Met	
	260 265 270	
20	aag cgc ctg aca gtg gcc cac cag cta cac cac agc ggc aag tac ggt	863
	Lys Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly	
	275 280 285	
	ggc gcg ccc tgg ggt atg ttc ttg ggt cca cag gag ctg cag cac att	911
	Gly Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile	
	290 295 300	
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	Pro Gly Ala Ala Glu Glu Val Glu Arg Leu Val Leu Glu Leu Asp Trp	
	305 310 315	
30	tcc aag cgg tag ggtgcggaac caggcacgct ggtttcacac ctcatgcctg	1011
	Ser Lys Arg	
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	tgataaggtg tggctagagc gatgcgtgtg agacgggtat gtcacggtcg actggtctga	1071
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	cacatcatca tgtgcggttg gaggggctgg cacagtgtgg gctgaactgg agcagttgtc	1191
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45	catgatgtac tcgtcatggt gtgttggtga gaggatggat gtggatggat gtgtattctc	1431

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 35 40 45
 Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser Leu
 50 55 60
 35 Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly Thr
 65 70 75 80
 40 Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala Leu
 85 90 95
 45 Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys Arg

	100	105	110
5	Glu Gln Leu Ser Tyr Gln Ala Ala Ala Ile Ala Ala Ser Ile Gly Val 115 120 125		
10	Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His Met 130 135 140		
15	Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu Leu 145 150 155 160		
20	Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr Ala 165 170 175		
25	His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His Lys 180 185 190		
30	Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu Phe 195 200 205		
35	Ala Ile Ile Asn Gly Leu Pro Ala Met Leu Leu Cys Thr Phe Gly Phe 210 215 220		
40	Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu Gly 225 230 235 240		
45	Ile Thr Leu Tyr Gly Met Ala Tyr Met Phe Val His Asp Gly Leu Val 245 250 255		
	His Arg Arg Phe Pro Thr Gly Pro Ile Ala Gly Leu Pro Tyr Met Lys 260 265 270		
	Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly Gly 275 280 285		

Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile Pro
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Lys Arg

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 1 5 10 15

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cat cat ggt ttt gct gtt aaa gct agt acc ttt aga tct gag aag cat 96
 His His Gly Phe Ala Val Lys Ala Ser Thr Phe Arg Ser Glu Lys His
 20 25 30

45

cat aat ttt ggt tct agg aag ttt tgt gaa act ttg ggt aga agt gtt 144
 His Asn Phe Gly Ser Arg Lys Phe Cys Glu Thr Leu Gly Arg Ser Val

	35	40	45	
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	50	55	60	
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	65	70	75	80
	ggg gtt gtt gtg gat ctt gct gtg gtt ggt ggt ggc cct gca gga ctt Gly Val Val Val Asp Leu Ala Val Val Gly Gly Gly Pro Ala Gly Leu	288		
	85	90	95	
15	gct gtt gca cag caa gtt tct gaa gca gga ctc tct gtt tgt tca att Ala Val Ala Gln Gln Val Ser Glu Ala Gly Leu Ser Val Cys Ser Ile	336		
	100	105	110	
20	gat ccg aat cct aaa ttg ata tgg cct aat aac tat ggt gtt tgg gtg Asp Pro Asn Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val Trp Val	384		
	115	120	125	
25	gat gaa ttt gag gct atg gac ttg tta gat tgt cta gat gct acc tgg Asp Glu Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Ala Thr Trp	432		
	130	135	140	
30	tct ggt gca gca gtg tac att gat gat aat acg gct aaa gat ctt cat Ser Gly Ala Ala Val Tyr Ile Asp Asp Asn Thr Ala Lys Asp Leu His	480		
	145	150	155	160
	aga cct tat gga agg gtt aac cgg aaa cag ctg aaa tcg aaa atg atg Arg Pro Tyr Gly Arg Val Asn Arg Lys Gln Leu Lys Ser Lys Met Met	528		
	165	170	175	
35	cag aaa tgt ata atg aat ggt gtt aaa ttc cac caa gcc aaa gtt ata Gln Lys Cys Ile Met Asn Gly Val Lys Phe His Gln Ala Lys Val Ile	576		
	180	185	190	
40	aag gtg att cat gag gaa tcg aaa tcc atg ttg ata tgc aat gat ggt Lys Val Ile His Glu Glu Ser Lys Ser Met Leu Ile Cys Asn Asp Gly	624		
	195	200	205	
45	att act att cag gca acg gtg gtg ctc gat gca act ggc ttc tct aga Ile Thr Ile Gln Ala Thr Val Val Leu Asp Ala Thr Gly Phe Ser Arg	672		
	210	215	220	

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	Ser Leu Val Gln Tyr Asp Lys Pro Tyr Asn Pro Gly Tyr Gln Val Ala	
	225 230 235 240	
5	tat ggc att ttg gct gaa gtg gaa gag cac ccc ttt gat gta aac aag	768
	Tyr Gly Ile Leu Ala Glu Val Glu Glu His Pro Phe Asp Val Asn Lys	
	245 250 255	
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	Met Val Phe Met Asp Trp Arg Asp Ser His Leu Lys Asn Asn Thr Asp	
	260 265 270	
	ctc aag gag aga aat agt aga ata cca act ttt ctt tat gca atg cca	864
15	Leu Lys Glu Arg Asn Ser Arg Ile Pro Thr Phe Leu Tyr Ala Met Pro	
	275 280 285	
	ttt tca tcc aac agg ata ttt ctt gaa gaa aca tca ctc gta gct cgt	912
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	cct ggc ttg cgt ata gat gat att caa gaa cga atg gtg gct cgt tta	960
	Pro Gly Leu Arg Ile Asp Asp Ile Gln Glu Arg Met Val Ala Arg Leu	
	305 310 315 320	
25	aac cat ttg ggg ata aaa gtg aag agc att gaa gaa gat gaa cat tgt	1008
	Asn His Leu Gly Ile Lys Val Lys Ser Ile Glu Glu Asp Glu His Cys	
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30	cta ata cca atg ggt ggt cca ctt cca gta tta cct cag aga gtc gtt	1056
	Leu Ile Pro Met Gly Gly Pro Leu Pro Val Leu Pro Gln Arg Val Val	
	340 345 350	
	gga atc ggt ggt aca gct ggc atg gtt cat cca tcc acc ggt tat atg	1104
35	Gly Ile Gly Gly Thr Ala Gly Met Val His Pro Ser Thr Gly Tyr Met	
	355 360 365	
	gtg gca agg aca cta gct gcg gct cct gtt gtt gcc aat gcc ata att	1152
	Val Ala Arg Thr Leu Ala Ala Ala Pro Val Val Ala Asn Ala Ile Ile	
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	caa tac ctc ggt tct gaa aga agt cat tcg ggt aat gaa tta tcc aca	1200
	Gln Tyr Leu Gly Ser Glu Arg Ser His Ser Gly Asn Glu Leu Ser Thr	
	385 390 395 400	
45		

45

	gct gtt tgg aaa gat ttg tgg cct ata gag agg aga cgt caa aga gag	1248
	Ala Val Trp Lys Asp Leu Trp Pro Ile Glu Arg Arg Arg Gln Arg Glu	
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5	ttc ttc tgc ttc ggt atg gat att ctt ctg aag ctt gat tta cct gct	1296
	Phe Phe Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu Pro Ala	
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10	aca aga agg ttc ttt gat gca ttc ttt gac tta gaa cct cgt tat tgg	1344
	Thr Arg Arg Phe Phe Asp Ala Phe Phe Asp Leu Glu Pro Arg Tyr Trp	
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15	cat ggc ttc tta tgc tct cga ttg ttt cta cct gaa ctc ata gtt ttt	1392
	His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Ile Val Phe	
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	Gly Leu Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Phe Glu Ile	
	465 470 475 480	
	atg aca aag gga act gtt cca tta gta aat atg atc aac aat ttg tta	1488
	Met Thr Lys Gly Thr Val Pro Leu Val Asn Met Ile Asn Asn Leu Leu	
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5 His Asn Phe Gly Ser Arg Lys Phe Cys Glu Thr Leu Gly Arg Ser Val
 35 40 45

10 Cys Val Lys Gly Ser Ser Ser Ala Leu Leu Glu Leu Val Pro Glu Thr
 50 55 60

15 Lys Lys Glu Asn Leu Asp Phe Glu Leu Pro Met Tyr Asp Pro Ser Lys
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Gly Val Val Val Asp Leu Ala Val Val Gly Gly Gly Pro Ala Gly Leu
 85 90 95

20 Ala Val Ala Gln Gln Val Ser Glu Ala Gly Leu Ser Val Cys Ser Ile
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25 Asp Pro Asn Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val Trp Val
 115 120 125

30 Asp Glu Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Ala Thr Trp
 130 135 140

35 Ser Gly Ala Ala Val Tyr Ile Asp Asp Asn Thr Ala Lys Asp Leu His
 145 150 155 160

Arg Pro Tyr Gly Arg Val Asn Arg Lys Gln Leu Lys Ser Lys Met Met
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40 Gln Lys Cys Ile Met Asn Gly Val Lys Phe His Gln Ala Lys Val Ile
 180 185 190

45 Lys Val Ile His Glu Glu Ser Lys Ser Met Leu Ile Cys Asn Asp Gly

	195	200	205
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10	Ser Leu Val Gln Tyr Asp Lys Pro Tyr Asn Pro Gly Tyr Gln Val Ala 225 230 235 240		
15	Tyr Gly Ile Leu Ala Glu Val Glu Glu His Pro Phe Asp Val Asn Lys 245 250 255		
20	Met Val Phe Met Asp Trp Arg Asp Ser His Leu Lys Asn Asn Thr Asp 260 265 270		
25	Leu Lys Glu Arg Asn Ser Arg Ile Pro Thr Phe Leu Tyr Ala Met Pro 275 280 285		
30	Phe Ser Ser Asn Arg Ile Phe Leu Glu Glu Thr Ser Leu Val Ala Arg 290 295 300		
35	Pro Gly Leu Arg Ile Asp Asp Ile Gln Glu Arg Met Val Ala Arg Leu 305 310 315 320		
40	Asn His Leu Gly Ile Lys Val Lys Ser Ile Glu Glu Asp Glu His Cys 325 330 335		
45	Leu Ile Pro Met Gly Gly Pro Leu Pro Val Leu Pro Gln Arg Val Val 340 345 350		
	Gly Ile Gly Gly Thr Ala Gly Met Val His Pro Ser Thr Gly Tyr Met 355 360 365		
	Val Ala Arg Thr Leu Ala Ala Ala Pro Val Val Ala Asn Ala Ile Ile 370 375 380		

5 Gln Tyr Leu Gly Ser Glu Arg Ser His Ser Gly Asn Glu Leu Ser Thr
385 390 395 400

10 Ala Val Trp Lys Asp Leu Trp Pro Ile Glu Arg Arg Arg Gln Arg Glu
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15 Phe Phe Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu Pro Ala
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20 Thr Arg Arg Phe Phe Asp Ala Phe Phe Asp Leu Glu Pro Arg Tyr Trp
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25 His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Ile Val Phe
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Gly Leu Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Phe Glu Ile
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<223>

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	Val Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser	
	35 40 45	
10	gac gcg gcc cgc ccg gga ctg aag aat gcc tac aag cca cca cct tcc	194
	Asp Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser	
	50 55 60	
15	gac aca aag ggc atc aca atg gcg cta gct gtc atc ggc tcc tgg gcc	242
	Asp Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp Ala	
	65 70 75	
20	gca gtg ttc ctc cac gcc att ttt caa atc aag ctt ccg acc tcc ttg	290
	Ala Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu	
	80 85 90 95	
	gac cag ctg cac tgg ctg ccc gtg tca gat gtc aca gct cag ctg gtt	338
	Asp Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val	
	100 105 110	
25	agc ggc agc agc agc ctg ctg cac atc gtc gta gta ttc ttt gtc ctg	386
	Ser Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu	
	115 120 125	
30	gag ttc ctg tac aca ggc ctt ttt atc acc acg cat gat gct atg cat	434
	Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His	
	130 135 140	
35	ggc acc atc gcc atg aga aac agg cag ctt aat gac ttc ttg ggc aga	482
	Gly Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg	
	145 150 155	
40	gta tgc atc tcc ttg tac gcc tgg ttt gat tac aac atg ctg cac cgc	530
	Val Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg	
	160 165 170 175	
	aag cat tgg gag cac cac aac cac act ggc gag gtg ggc aag gac cct	578
	Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro	
	180 185 190	
45	gac ttc cac agg gga aac cct ggc att gtg ccc tgg ttt gcc agc ttc	626

51

	Asp	Phe	His	Arg	Gly	Asn	Pro	Gly	Ile	Val	Pro	Trp	Phe	Ala	Ser	Phe	
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	atg	tcc	agc	tac	atg	tcg	atg	tgg	cag	ttt	gcg	cgc	ctc	gca	tgg	tgg	674
5	Met	Ser	Ser	Tyr	Met	Ser	Met	Trp	Gln	Phe	Ala	Arg	Leu	Ala	Trp	Trp	
			210					215					220				
	acg	gtg	gtc	atg	cag	ctg	ctg	ggc	gcg	cca	atg	gcg	aac	ctg	ctg	gtg	722
10	Thr	Val	Val	Met	Gln	Leu	Leu	Gly	Ala	Pro	Met	Ala	Asn	Leu	Leu	Val	
			225					230					235				
	ttc	atg	gcg	gcc	gcg	ccc	atc	ctg	tcc	gcc	ttc	cgc	ttg	ttc	tac	ttt	770
	Phe	Met	Ala	Ala	Ala	Pro	Ile	Leu	Ser	Ala	Phe	Arg	Leu	Phe	Tyr	Phe	
	240					245					250				255		
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	Gly	Thr	Tyr	Met	Pro	His	Lys	Pro	Glu	Pro	Gly	Ala	Ala	Ser	Gly	Ser	
					260					265					270		
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	Ser	Pro	Ala	Val	Met	Asn	Trp	Trp	Lys	Ser	Arg	Thr	Ser	Gln	Ala	Ser	
				275					280					285			
	gac	ctg	gtc	agc	ttt	ctg	acc	tgc	tac	cac	ttc	gac	ctg	cac	tgg	gag	914
25	Asp	Leu	Val	Ser	Phe	Leu	Thr	Cys	Tyr	His	Phe	Asp	Leu	His	Trp	Glu	
			290					295					300				
	cac	cac	cgc	tgg	ccc	ttt	gcc	ccc	tgg	tgg	gag	ctg	ccc	aac	tgc	cgc	962
30	His	His	Arg	Trp	Pro	Phe	Ala	Pro	Trp	Trp	Glu	Leu	Pro	Asn	Cys	Arg	
			305				310					315					
	cgc	ctg	tct	ggc	cga	ggc	ctg	gtt	cct	gcc	tag	ctggacacac	tgacagtgggc				1015
	Arg	Leu	Ser	Gly	Arg	Gly	Leu	Val	Pro	Ala							
	320					325											
35	cctgctgccca	gctgggcatg	cagggttgtgg	caggactggg	tgaggtgaaa	agctgcaggc											1075
	gctgctgccg	gacacgctgc	atgggctacc	ctgtgtagct	gccgccacta	ggggaggggg											1135
40	ttttagctg	tcgagcttgc															1155

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<212> PRT

5 <213> Haematococcus pluvialis

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Met Gln Leu Ala Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala
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Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val
 20 25 30

20

Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp
 35 40 45

25

Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp
 50 55 60

30

Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp Ala Ala
 65 70 75 80

35

Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp
 85 90 95

40

Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser
 100 105 110

Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu Glu
 115 120 125

45

Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly
 130 135 140

Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val
 145 150 155 160

5

Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys
 165 170 175

10

His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp
 180 185 190

15

Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met
 195 200 205

20

Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr
 210 215 220

25

Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe
 225 230 235 240

30

Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly
 245 250 255

35

Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser
 260 265 270

40

Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp
 275 280 285

45

Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His
 290 295 300

His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg
 305 310 315 320

Leu Ser Gly Arg Gly Leu Val Pro Ala
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5 <210> 24

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<222> (4)..(951)

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30 tct gac gtg ttg cgt aca tgg gcg acc cag tac tcg ctt ccg tca gaa 96

Ser Asp Val Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu	
20 25 30	

35 gag tca gac gcg gcc cgc ccg gga ctg aag aat gcc tac aag cca cca 144

Glu Ser Asp Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro	
35 40 45	

40 cct tcc gac aca aag ggc atc aca atg gcg cta gct gtc atc ggc tcc 192

Pro Ser Asp Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser	
50 55 60	

45 tgg gcc gca gtg ttc ctc cac gcc att ttt caa atc aag ctt ccg acc 240

Trp Ala Ala Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr	
65 70 75	

55

	tcc ttg gac cag ctg cac tgg ctg ccc gtg tca gat gcc aca gct cag	288
	Ser Leu Asp Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln	
	80 85 90 95	
5	ctg gtt agc ggc agc agc agc ctg ctg cac atc gtc gta gta ttc ttt	336
	Leu Val Ser Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe	
	100 105 110	
10	gtc ctg gag ttc ctg tac aca ggc ctt ttt atc acc acg cat gat gct	384
	Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala	
	115 120 125	
15	atg cat ggc acc atc gcc atg aga aac agg cag ctt aat gac ttc ttg	432
	Met His Gly Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu	
	130 135 140	
20	ggc aga gta tgc atc tcc ttg tac gcc tgg ttt gat tac aac atg ctg	480
	Gly Arg Val Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu	
	145 150 155	
	cac cgc aag cat tgg gag cac cac aac cac act ggc gag gtg ggc aag	528
	His Arg Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys	
	160 165 170 175	
25	gac cct gac ttc cac agg gga aac cct ggc att gtg ccc tgg ttt gcc	576
	Asp Pro Asp Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala	
	180 185 190	
30	agc ttc atg tcc agc tac atg tcg atg tgg cag ttt gcg cgc ctc gca	624
	Ser Phe Met Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala	
	195 200 205	
35	tgg tgg acg gtg gtc atg cag ctg ctg ggt gcg cca atg gcg aac ctg	672
	Trp Trp Thr Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu	
	210 215 220	
40	ctg gtg ttc atg gcg gcc gcg ccc atc ctg tcc gcc ttc cgc ttg ttc	720
	Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe	
	225 230 235	
	tac ttt ggc acg tac atg ccc cac aag cct gag cct ggc gcc gcg tca	768
	Tyr Phe Gly Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser	
	240 245 250 255	
45	ggc tct tca cca gcc gtc atg aac tgg tgg aag tcg cgc act agc cag	816

56

Gly Ser Ser Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln
 260 265 270

5 gcg tcc gac ctg gtc agc ttt ctg acc tgc tac cac ttc gac ctg cac 864
 Ala Ser Asp Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His
 275 280 285

10 tgg gag cac cac cgc tgg ccc ttc gcc ccc tgg tgg gag ctg ccc aac 912
 Trp Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn
 290 295 300

tgc cgc cgc ctg tct ggc cga ggt ctg gtt cct gcc tag ctggacacac 961
 Cys Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala
 305 310 315

15 tgcagtgggc cctgctgcca gctgggcatg caggttgtgg caggactggg tgaggtgaaa 1021
 agctgcaggc gctgctgccg gacacgttgc atgggctacc ctgtgtagct gccgccacta 1081

20 ggggagggggg tttgtagctg tcgagcttgc 1111

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25 <211> 315

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<213> Haematococcus pluvialis

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35 Met Leu Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser
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40 Asp Val Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu
 20 25 30

Ser Asp Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro
 35 40 45

45

Ser Asp Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp
 50 55 60

5

Ala Ala Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser
 65 70 75 80

10

Leu Asp Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu
 85 90 95

15

Val Ser Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val
 100 105 110

20

Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met
 115 120 125

His Gly Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly
 130 135 140

25

Arg Val Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His
 145 150 155 160

30

Arg Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp
 165 170 175

35

Pro Asp Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser
 180 185 190

40

Phe Met Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp
 195 200 205

Trp Thr Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu
 210 215 220

45

58

'225

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305

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<21

<21

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<22.

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59

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	Met Gln Leu Ala Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser	
	1 5 10 15	
5	gct gag gca ctc aag gag aag gag aag gag gtt gca ggc agc tct gac	98
	Ala Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp	
	20 25 30	
	gtg ttg cgt aca tgg gcg acc cag tac tgg ctt ccg tca gag gag tca	146
10	Val Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser	
	35 40 45	
	gac gcg gcc cgc ccg gga ctg aag aat gcc tac aag cca cca cct tcc	194
15	Asp Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser	
	50 55 60	
	gac aca aag ggc atc aca atg gcg cta gct gtc atc ggc tcc tgg gct	242
	Asp Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp Ala	
	65 70 75	
20	gca gtg ttc ctc cag gcc att ttt caa atc aag ctt ccg acc tcc ttg	290
	Ala Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu	
	80 85 90 95	
25	gac cag ctg cac tgg ctg ccc gtg tca gat gcc aca gct cag ctg gtt	338
	Asp Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val	
	100 105 110	
	agc ggc agc agc agc ctg ctg cac atc gtc gta gta ttc ttt gtc ctg	386
30	Ser Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu	
	115 120 125	
	gag ttc ctg tac aca ggc ctt ttt atc acc acg cat gat gct atg cat	434
35	Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His	
	130 135 140	
	ggc acc atc gcc atg aga aac agg cag ctt aat gac ttc ttg ggc aga	482
	Gly Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg	
	145 150 155	
40	gta tgc atc tcc ttg tac gcc tgg ttt gat tac aac atg ctg cac cgc	530
	Val Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg	
	160 165 170 175	
45	aag cat tgg gag cac cac aac cac act ggc gag gtg ggc aag gac cct	578

60

	Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro	
	180	185 190
5	gac ttc cac agg gga aac cct ggc att gtg ccc tgg ttt gcc agc ttc Asp Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe	626
	195 200 205	
10	atg tcc agc tac atg tcg atg tgg cag ttt gcg cgc ctc gca tgg tgg Met Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp	674
	210 215 220	
15	acg gtg gtc atg cag ctg ctg ggt gcg cca atg gcg aac ctg ctg gtg Thr Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val	722
	225 230 235	
20	ttc atg gcg gcc gcg ccc atc ctg tcc gcc ttc cgc ttg ttc tac ttt Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe	770
	240 245 250 255	
25	ggc acg tac atg ccc cac aag cct gag cct ggc gcc gcg tca ggc tct Gly Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser	818
	260 265 270	
30	tca cca gcc gtc atg aac tgg tgg aag tcg cgc act agc cag gcg tcc Ser Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser	866
	275 280 285	
35	gac ctg gtc agc ttt ctg acc tgc tac cac ttc gac ctg cac tgg gag Asp Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu	914
	290 295 300	
40	cac cac cgc tgg ccc ttt gcc ccc tgg tgg gag ctg ccc aac tgc cgc His His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg	962
	305 310 315	
45	cgc ctg tct ggc cga ggt ctg gtt cct gcc gag caa aaa ctc atc tca Arg Leu Ser Gly Arg Gly Leu Val Pro Ala Glu Gln Lys Leu Ile Ser	1010
	320 325 330 335	
50	gaa gag gat ctg aat agc tag Glu Glu Asp Leu Asn Ser	1031
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<211> 341

5 <212> PRT

<213> Haematococcus pluvialis

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Met Gln Leu Ala Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala
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Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val
 20 25 30

20

Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp
 35 40 45

25

Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp
 50 55 60

30

Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp Ala Ala
 65 70 75 80

35

Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp
 85 90 95

40

Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser
 100 105 110

Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu Glu
 115 120 125

45

Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly

	130		135		140
	Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val				
5	145		150		155 160
	Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys				
10		165		170	175
	His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp				
		180		185	190
15	Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met				
		195		200	205
20	Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr				
		210		215	220
	Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe				
25		225		230	235 240
	Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly				
30		245		250	255
	Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser				
		260		265	270
35	Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp				
		275		280	285
40	Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His				
		290		295	300
	His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg				
45		305		310	315 320

Leu Ser Gly Arg Gly Leu Val Pro Ala Glu Gln Lys Leu Ile Ser Glu
 325 330 335

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Glu Asp Leu Asn Ser
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<211> 777

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<221> promoter

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tagtttcaaa acaacagtaa ctgtggccaa cttagttttg aaacaacact aactgggtcga 120

35

agcaaaaaga aaaaagagtt tcatcatata tctgatttga tggactgttt ggagtttagga 180

ccaaacatta tctacaaaca aagacttttc tcctaacttg tgattccttc ttaaacccta 240

40

ggggtaatat tctattttcc aaggatcttt agttaaaggc aaatccggga aattattgta 300

atcatttggg gaaacatata aaagatttga gttagatgga agtgacgatt aatccaaaca 360

tatatatctc tttcttctta tttcccaaata taacagacaa aagtagaata ttggctttta 420

45

64

acaccaatat aaaaacttgc ttcacaccta aacacttttg tttacttttag ggtaagtgca 480
aaaagccaac caaatccacc tgcactgatt tgacgtttac aaacgccgtt aagtcgatgt 540
5 ccgttgattt aaacagtgtc ttgtaattaa aaaaatcagt ttacataaat ggaaaattta 600
tcacttagtt ttcatcaact tctgaactta cttttcatgg attaggcaat actttccatt 660
tttagtaact caagtggacc ctttacttct tcaactccat ctctctcttt ctatttcact 720
10 tctttcttct cattatatct cttgtcctct ccaccaaate tttcaacaa aaagctt 777
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15 <211> 22
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20 <213> artificial
<220>
25 <221> primer_bind
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30 <223>
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35 gcaagctcga cagctacaaa cc 22
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<210> 31

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<210> 32

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24

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<222> (1)..(28)

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<210> 36

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<211> 25

<212> DNA

10

<213> artificial

<220>

15

<221> primer_bind

<222> (1)..(25)

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<223>

<400> 36

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taagcttttt gttgaagaga tttgg

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<210> 37

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<211> 212

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<213> Artificial sequence

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<220>

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<221> Intron

<222> (1)..(212)

<223>

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 gcttttctgt agtttataag tgtgtatatt ttaatttata acttttctaa tatatgacca 180
 10 aaatttggtg atgtgcaggt atcacggat cc 212

<210> 38
 15 <211> 1830
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 25 <221> CDS
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 agaatcatta ctaacaatca atg agt atg aga gct gga cac atg acg gca aca 173
 Met Ser Met Arg Ala Gly His Met Thr Ala Thr
 40 1 5 10
 atg gcg gct ttt aca tgc cct agg ttt atg act agc atc aga tac acg 221
 Met Ala Ala Phe Thr Cys Pro Arg Phe Met Thr Ser Ile Arg Tyr Thr
 15 20 25
 45

70

	aag caa att aag tgc aac gct gct aaa agc cag cta gtc gtt aaa caa	269
	Lys Gln Ile Lys Cys Asn Ala Ala Lys Ser Gln Leu Val Val Lys Gln	
	30 35 40	
5	gag att gag gag gaa gaa gat tat gtg aaa gcc ggt gga tcg gag ctg	317
	Glu Ile Glu Glu Glu Glu Asp Tyr Val Lys Ala Gly Gly Ser Glu Leu	
	45 50 55	
10	ctt ttt gtt caa atg caa cag aat aag tcc atg gat gca cag tct agc	365
	Leu Phe Val Gln Met Gln Gln Asn Lys Ser Met Asp Ala Gln Ser Ser	
	60 65 70 75	
15	cta tcc caa aag ctc cca agg gta cca ata gga gga gga gga gac agt	413
	Leu Ser Gln Lys Leu Pro Arg Val Pro Ile Gly Gly Gly Gly Asp Ser	
	80 85 90	
20	aac tgt ata ctg gat ttg gtt gta att ggt tgt ggt cct gct ggc ctt	461
	Asn Cys Ile Leu Asp Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu	
	95 100 105	
25	gct ctt gct gga gaa tca gcc aag cta ggc ttg aat gtc gca ctt atc	509
	Ala Leu Ala Gly Glu Ser Ala Lys Leu Gly Leu Asn Val Ala Leu Ile	
	110 115 120	
30	ggc cct gat ctt cct ttt aca aat aac tat ggt gtt tgg gag gat gaa	557
	Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu	
	125 130 135	
35	ttt ata ggt ctt gga ctt gag ggc tgt att gaa cat gtt tgg cga gat	605
	Phe Ile Gly Leu Gly Leu Glu Gly Cys Ile Glu His Val Trp Arg Asp	
	140 145 150 155	
40	act gta gta tat ctt gat gac aac gat ccc att ctc ata ggt cgt gcc	653
	Thr Val Val Tyr Leu Asp Asp Asn Asp Pro Ile Leu Ile Gly Arg Ala	
	160 165 170	
45	tat gga cga gtt agt cgt gat tta ctt cac gag gag ttg ttg act agg	701
	Tyr Gly Arg Val Ser Arg Asp Leu Leu His Glu Glu Leu Leu Thr Arg	
	175 180 185	
50	tgc atg gag tca ggc gtt tca tat ctg agc tcc aaa gtg gaa cgg att	749
	Cys Met Glu Ser Gly Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile	
	190 195 200	
55	act gaa gct cca aat ggc cta agt ctc ata gag tgt gaa ggc aat atc	797

	Thr Glu Ala Pro Asn Gly Leu Ser Leu Ile Glu Cys Glu Gly Asn Ile	
	205 210 215	
5	aca att cca tgc agg ctt gct act gtc gct tct gga gca gct tct gga Thr Ile Pro Cys Arg Leu Ala Thr Val Ala Ser Gly Ala Ala Ser Gly	845
	220 225 230 235	
10	aaa ctt ttg cag tat gaa ctt ggc ggt ccc cgt gtt tgc gtt caa aca Lys Leu Leu Gln Tyr Glu Leu Gly Gly Pro Arg Val Cys Val Gln Thr	893
	240 245 250	
15	gct tat ggt ata gag gtt gag gtt gaa agc ata ccc tat gat cca agc Ala Tyr Gly Ile Glu Val Glu Val Glu Ser Ile Pro Tyr Asp Pro Ser	941
	255 260 265	
	cta atg gtt ttc atg gat tat aga gac tac acc aaa cat aaa tct caa Leu Met Val Phe Met Asp Tyr Arg Asp Tyr Thr Lys His Lys Ser Gln	989
	270 275 280	
20	tca cta gaa gca caa tat cca aca ttt ttg tat gtc atg cca atg tct Ser Leu Glu Ala Gln Tyr Pro Thr Phe Leu Tyr Val Met Pro Met Ser	1037
	285 290 295	
25	cca act aaa gta ttc ttt gag gaa act tgt ttg gct tca aaa gag gcc Pro Thr Lys Val Phe Phe Glu Glu Thr Cys Leu Ala Ser Lys Glu Ala	1085
	300 305 310 315	
30	atg cct ttt gag tta ttg aag aca aaa ctc atg tca aga tta aag act Met Pro Phe Glu Leu Leu Lys Thr Lys Leu Met Ser Arg Leu Lys Thr	1133
	320 325 330	
35	atg ggg atc cga ata acc aaa act tat gaa gag gaa tgg tca tat att Met Gly Ile Arg Ile Thr Lys Thr Tyr Glu Glu Glu Trp Ser Tyr Ile	1181
	335 340 345	
	cca gta ggt gga tcc tta cca aat acc gag caa aag aac ctt gca ttt Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Lys Asn Leu Ala Phe	1229
	350 355 360	
40	ggt gct gct gct agc atg gtg cat cca gcc aca gga tat tcg gtt gta Gly Ala Ala Ala Ser Met Val His Pro Ala Thr Gly Tyr Ser Val Val	1277
	365 370 375	
45	aga tca ctg tca gaa gct cct aat tat gca gca gta att gca aag att Arg Ser Leu Ser Glu Ala Pro Asn Tyr Ala Ala Val Ile Ala Lys Ile	1325

	380	385	390	395	
	tta ggg aaa gga aat tca aaa cag atg ctt gat cat gga aga tac aca				1373
	Leu Gly Lys Gly Asn Ser Lys Gln Met Leu Asp His Gly Arg Tyr Thr				
5	400		405	410	
	acc aac atc tca aag caa gct tgg gaa aca ctt tgg ccc ctt gaa agg				1421
	Thr Asn Ile Ser Lys Gln Ala Trp Glu Thr Leu Trp Pro Leu Glu Arg				
10	415	420	425		
	aaa aga cag aga gca ttc ttt ctc ttt gga tta gca ctg att gtc cag				1469
	Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln				
	430	435	440		
15	atg gat att gag ggg acc cgc aca ttc ttc cgg act ttc ttc cgc ttg				1517
	Met Asp Ile Glu Gly Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu				
	445	450	455		
	ccc aca tgg atg tgg tgg ggg ttt ctt gga tct tcg tta tca tca act				1565
20	Pro Thr Trp Met Trp Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr				
	460	465	470	475	
	gac ttg ata ata ttt gcg ttt tac atg ttt atc ata gca ccg cat agc				1613
	Asp Leu Ile Ile Phe Ala Phe Tyr Met Phe Ile Ile Ala Pro His Ser				
25	480	485	490		
	ctg aga atg ggt ctg gtt aga cat ttg ctt tct gac ccg aca gga gga				1661
	Leu Arg Met Gly Leu Val Arg His Leu Leu Ser Asp Pro Thr Gly Gly				
30	495	500	505		
	aca atg tta aaa gcg tat ctc acg ata taa ataactctag tcgcgatcag				1711
	Thr Met Leu Lys Ala Tyr Leu Thr Ile				
	510	515			
35	tttagattat aggcacatct tgcatatata tatgtataaa ccttatgtgt gctgtatcct				1771
	tacatcaaca cagtcattaa ttgtatttct tggggtaatg ctgatgaagt attttctgg				1830
40	<210> 39				
	<211> 516				
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45					

<213> Tagetes erecta

5 <400> 39

Met Ser Met Arg Ala Gly His Met Thr Ala Thr Met Ala Ala Phe Thr
 1 5 10 15

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Cys Pro Arg Phe Met Thr Ser Ile Arg Tyr Thr Lys Gln Ile Lys Cys
 20 25 30

15

Asn Ala Ala Lys Ser Gln Leu Val Val Lys Gln Glu Ile Glu Glu Glu
 35 40 45

20

Glu Asp Tyr Val Lys Ala Gly Gly Ser Glu Leu Leu Phe Val Gln Met
 50 55 60

25

Gln Gln Asn Lys Ser Met Asp Ala Gln Ser Ser Leu Ser Gln Lys Leu
 65 70 75 80

30

Pro Arg Val Pro Ile Gly Gly Gly Gly Asp Ser Asn Cys Ile Leu Asp
 85 90 95

Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Gly Glu
 100 105 110

35

Ser Ala Lys Leu Gly Leu Asn Val Ala Leu Ile Gly Pro Asp Leu Pro
 115 120 125

40

Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Ile Gly Leu Gly
 130 135 140

45

Leu Glu Gly Cys Ile Glu His Val Trp Arg Asp Thr Val Val Tyr Leu
 145 150 155 160

Asp Asp Asn Asp Pro Ile Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser
 165 170 175

5 Arg Asp Leu Leu His Glu Glu Leu Leu Thr Arg Cys Met Glu Ser Gly
 180 185 190

10 Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile Thr Glu Ala Pro Asn
 195 200 205

15 Gly Leu Ser Leu Ile Glu Cys Glu Gly Asn Ile Thr Ile Pro Cys Arg
 210 215 220

20 Leu Ala Thr Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr
 225 230 235 240

Glu Leu Gly Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Ile Glu
 245 250 255

25 Val Glu Val Glu Ser Ile Pro Tyr Asp Pro Ser Leu Met Val Phe Met
 260 265 270

30 Asp Tyr Arg Asp Tyr Thr Lys His Lys Ser Gln Ser Leu Glu Ala Gln
 275 280 285

35 Tyr Pro Thr Phe Leu Tyr Val Met Pro Met Ser Pro Thr Lys Val Phe
 290 295 300

40 Phe Glu Glu Thr Cys Leu Ala Ser Lys Glu Ala Met Pro Phe Glu Leu
 305 310 315 320

Leu Lys Thr Lys Leu Met Ser Arg Leu Lys Thr Met Gly Ile Arg Ile
 325 330 335

45

Thr Lys Thr Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser
 340 345 350

5 Leu Pro Asn Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser
 355 360 365

10 Met Val His Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu
 370 375 380

15 Ala Pro Asn Tyr Ala Ala Val Ile Ala Lys Ile Leu Gly Lys Gly Asn
 385 390 395 400

Ser Lys Gln Met Leu Asp His Gly Arg Tyr Thr Thr Asn Ile Ser Lys
 405 410 415

20 Gln Ala Trp Glu Thr Leu Trp Pro Leu Glu Arg Lys Arg Gln Arg Ala
 420 425 430

25 Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln Met Asp Ile Glu Gly
 435 440 445

30 Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu Pro Thr Trp Met Trp
 450 455 460

35 Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr Asp Leu Ile Ile Phe
 465 470 475 480

Ala Phe Tyr Met Phe Ile Ile Ala Pro His Ser Leu Arg Met Gly Leu
 485 490 495

40 Val Arg His Leu Leu Ser Asp Pro Thr Gly Gly Thr Met Leu Lys Ala
 500 505 510

45 Tyr Leu Thr Ile

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 <212> DNA
 10 <213> Tagetes erecta
 <220>
 15 <221> Sense fragment
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 gaaaaagaat cattactaac aatcaatgag tatgagagct ggacacatga cggcaacaat 180
 30 ggcggtttt acatgcccta ggtttatgac tagcatcaga tacacgaagc aaattaagtg 240
 caacgtgtgt aaaagccagc tagtcgttaa acaagagatt gaggaggaag aagattatgt 300
 35 gaaagccggt ggatcggagc tgctttttgt tcaaagcaa cagaataagt ccatggatgc 360
 acagtctagc ctatcccaaa agctcccaag ggtaccaata ggaggaggag gagacagtaa 420
 ctgtatactg gatttggttg tcgac 445
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 <210> 41
 <211> 446
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<212> DNA

<213> *Tagetes erecta*

5

<220>

<221> Antisense fragment

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<222> (1)..(446)

<223>

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gaattcgcac gaggcaaagc aaagggttgtt tgttggttgtt gttgagagac actccaatcc 60

20 aaacagatac aaggcgtgac tggatatttc tctctcgttc ctaacaacag caacgaagaa 120

gaaaaagaat cattactaac aatcaatgag tatgagagct ggacacatga cggcaacaat 180

ggcggctttt acatgcccta ggtttatgac tagcatcaga tacacgaagc aaattaagtg 240

25 caacgctgct aaaagccagc tagtcgttaa acaagagatt gaggaggaag aagattatgt 300

gaaagccggt ggatcggagc tgctttttgt tcaaatgcaa cagaataagt ccatggatgc 360

30 acagtctagc ctatcccaaa agtcccaag ggtaccaata ggaggaggag gagacagtaa 420

ctgtatactg gatttggttg gatcct 446

35 <210> 42

<211> 393

<212> DNA

40

<213> *Tagetes erecta*

<220>

<221> Sense fragment

5 <222> (1)..(393)

<223>

10

<400> 42

aagcttttga ttagcactga ttgtccagat ggatattgag gggacccgca cattcttccg 60

gactttcttc cgcttgccca catggatgtg gtgggggttt cttggatctt cgttatcatc 120

15

aactgacttg ataatatattg cgttttacat gtttatcata gcaccgcata gcctgagaat 180

gggtctggtt agacatttgc tttctgaccc gacaggagga acaatgttaa aagcgtatct 240

20

cacgatataa ataactctag tcgcgatcag tttagattat aggcacatct tgcatatata 300

tatgtataaa ccttatgtgt gctgtatcct tacatcaaca cagtcattaa ttgtatttct 360

tggggtaatg ctgatgaagt attttctgtc gac 393

25

<210> 43

<211> 397

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<212> DNA

<213> Tagetes erecta

35

<220>

<221> Antisense fragment

40

<222> (1)..(397)

<223>

<400> 43'
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tccggacttt cttccgcttg cccacatgga tgtgggtggg gtttcttgga tcttcgttat 120
catcaactga cttgataata tttgcgtttt acatgtttat catagcaccg catagcctga 180
10 gaatgggtct ggtagacat ttgctttctg acccgacagg aggaacaatg ttaaaagcgt 240
atctcacgat ataaataact ctagtgcga tcagtttaga ttataggcac atcttgcata 300
tatatatgta taaaccttat gtgtgctgta tccttacatc aacacagtca ttaattgtat 360
15 ttcttggggg aatgctgatg aagtattttc tggatcc 397

<210> 44

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<211> 1537

<212> DNA

25 <213> -

<220>

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<221> promoter

<222> (1)..(1537)

35 <223>

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tgtacattta ttcaataata ttatatgttt attacaaatt ctcaatttct tattcatacc 120
tattcactca agcctttacc atcttccttt tctatttcaa tactatttct acttcatttt 180
45

	tcacgttttt aacatctttc tttatttctt gtccacttcg tttagggatg cctaagtcc	240
	caaatttcat ctctcgtagt aacacaaaac caatgtaatg ctacttctct ctacattttt	300
5	aatacaaata aagtgaaca aaatatctat aaataaaca atatatatat tttgttagac	360
	gctgtctcaa cccatcaatt aaaaaatttt gttatatttc tactttacct actaaatttg	420
10	tttctcatat ttacctttta acccccacaa aaaaaaatta taaaaaagaa agaaaaaagc	480
	taaaccctat ttaaatagtc aactataaga tcttaaaatt atcctcatca gtgtatagtt	540
	taattggta ttaacttata acattatata tctatgacat atactctctc ctagctattt	600
15	ctcacatttt ttaacttaag aaaatagtca taacatagtc taaaattcaa acatccacat	660
	gctctaattt gattaacaaa aagttagaaa tattttattt aataaaaaag actaataaat	720
20	atataaaatg aatgttcata cgcagacca tttagagatg agtatgcttt cacatgctga	780
	gattattttc aaaactaagg ttgtagcaat attaaatcaa taaaattatt ataaataaca	840
	aaattaacct gctcgtgttt gctgtatatg ggaggctaca aaataaatta aactaaagat	900
25	gattatgttt tagacatttt ttctatctgt attagtttat acatattaat tcaggagctg	960
	cacaacccaa ttctattttc gttccttggt ggctgggttt ctcacaaggt tcaatagtca	1020
30	atattagggt ttattggact tttaatagta tcaaacaaat ctatgtgtga acttaaaaat	1080
	tgtattaaat atttagggta acctgttgcc gtttttagaa taatgtttct tcttaataca	1140
	cgaaagcgta ttgtgtattc attcatttgg cgctcacat gcttcggttg gctcgttta	1200
35	gtctctgcct tctttgtata ttgtactccc cctcttcta tgccacgtgt tctgagctta	1260
	acaagccacg ttgcgtgcca ttgccaaaca agtcatttta acttcacaag gtccgatttg	1320
40	acctcaaaaa caacgacaag tttccgaaca gtcgcgaaga tcaagggtat aatcgtcttt	1380
	ttgaattcta tttctcttta tttaatagtc cctctcgtgt gatagttttt aaaagatttt	1440
	taaaacgtag ctgctgttta agtaaattccc agtccttcag tttgtgcttt tgtgtgtttt	1500
45	gtttctctga tttacggaat ttggaaataa taagctt	1537

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5 <211> 734

<212> DNA

10 <213> Artificial sequence

<220>

15 <221> variation

<222> (1)..(734)

20 <223>

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	cctagggttta tgactagcat cagatacacg aagcaaatta agtgcaacgc tgctaaaagc	120
	cagctagtcg ttaaacaaga gattgaggag gaagaagatt atgtgaaagc cggtaggatcg	180
30	gagctgcttt ttgttcaaat gcaacagaat aagtccatgg atgcacagtc tagcctatcc	240
	caaaagggtca ctccagactt aattgcttat aaataaataa atatgttttt taggaataat	300
	gatattttaga tagattagct atcacctgtg ctgtggtgtg cagctcccaa gggctcttacc	360
35	gatagtaaaa tcgttagtta tgattaatac ttgggagggtg ggggattata ggctttgttg	420
	tgagaatggt gagaaagagg ttgacaaat cgggtgtttga atgaggttaa atggagtta	480
40	attaaaataa agagaagaga aagattaaga ggggtgatggg gatattaaag acggscaata	540
	tagtgatgcc acgtagaaaa aggtaagtga aaacatacaa cgtggcttta aaagatggct	600
45	tggtctgtaa tcaactcaac tcaactcata tcctatccat tcaaattcaa ttcaattcta	660

ttgaatgcaa agcaaagcaa aggttggttg ttggtgtgtg tgagagacac tccaatccaa 720
 acagatacaa ggcg 734

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<210> 46

<211> 280

10 <212> DNA

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<220>

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attaaagacg gccaatrtag tgatgccacg taagaaaaag gtaagtgaaa acatacaacg 120

30 tggcgtttaa agatggcttg gctgctaata aactcaactc aactcatatc ctatccattc 180

aaattcaatt caattctatt gaatgcaaag caaagcaaag caaagggtgt ttggtgtgtg 240

35 tgttgagaga cactccaatc caaacagata caaggcgtga 280

<210> 47

40 <211> 358

<212> DNA

<213> Tagetes erecta

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<220>

5 <221> Sense promoter

<222> (1)..(358)

<223>

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<400> 47

15 aagcttaccg atagtaaaat cgtaggttat gattaatact tgggaggtgg gggattatag 60

gctttgttgt gagaatgttg agaaagaggt ttgacaaatc ggtgtttgaa tgagggttaa 120

tggagtttaa ttaaaataaa gagaagagaa agattaagag ggtgatgggg atattaaaga 180

20 cggccaatat agtgatgcca cgtagaaaaa ggtaagtga aacatacaac gtggctttaa 240

aagatggctt ggctgcta at caactcaact caactcatat cctatccatt caaattcaat 300

25 tcaattctat tgaatgcaaa gcaaagcaaa gcaaagggtg tttgttgtg ttgtcgac 358

<210> 48

<211> 361

30 <212> DNA

<213> Tagetes erecta

35

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40 <222> (1)..(361)

<223>

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taggctttgt tgtgagaatg ttgagaaaga ggtttgacaa atcgggtgtt gaatgagggt 120
aaatggagtt taattaaaat aaagagaaga gaaagattaa gagggatgat gggatattaa 180
10 agacggccaa tatagtgatg ccacgtagaa aaaggtaagt gaaaacatac aacgtggctt 240
taaaagatgg cttggctgct aatcaactca actcaactca taccctatcc attcaaattc 300
15 aattcaattc tattgaatgc aaagcaaagc aaagcaaagg ttgtttgttg ttgttggatc 360
c 361

<210> 49
20 <211> 28
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25 <213> Artificial sequence

<220>
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<222> (1) ... (28)
35 <223>

<400> 49
40 gagctcactc actgatttcc attgcttg 28

<210> 50

<211> 37

<212> DNA

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<222> (1)..(37)

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25 <211> 34

<212> DNA

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<220>

35 <221> Primer

<222> (1)..(34)

<223>

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<400> 51

45 atcaacggac atcgacttaa cggcgtttgt aaac

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5 <210> 52
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15 <222> (1)..(25)
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<400> 52
taagcttttt gttgaagaga tttgg

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<210> 53
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30 <212> DNA
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<220>
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<400> 53
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5 <210> 54

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15 <220>

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<222> (1)..(28)
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25 <400> 54
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30 <210> 55

<211> 26

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40 <220>

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<222> (1)..(26)
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26

<210> 56

10 <211> 28

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28

<210> 57

35 <211> 29

<212> DNA

40 <213> Artificial sequence

<220>

45 <221> Primer

<222> (1)..(29)

<223>

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<400> 57

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29

10

<210> 58

<211> 30

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<212> DNA

<213> Artificial sequence

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<220>

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<222> (1)..(30)

<223>

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<400> 58

aggatccaac caaatccagt atacagttac

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35

<210> 59

<211> 28

<212> DNA

40

<213> Artificial sequence

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<223>

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<400> 59

gaattcgcac gaggcaaagc aaagggttg

28

15 <210> 60

<211> 25

<212> DNA

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<221> Primer

<222> (1)..(25)

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<223>

35 <400> 60

aagctttgga ttagcactga ttgtc

25

40

<210> 61

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<212> DNA

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5 <220>

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<222> (1)..(29)

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29

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<211> 29

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<210> 63

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<222> (1)..(27)

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27

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 <210> 66
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30 <212> DNA
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<400> 66
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26

5 <210> 67

<211> 26

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<222> (1)..(26)

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<223>

25 <400> 67

ccttgggagc ttttgggata ggctag

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<210> 68

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<212> DNA

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<221> Primer

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45 <223>

5 <400> 68
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10 <210> 69
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<212> DNA

15 <213> Artificial sequence

<220>

20 <221> Primer

<222> (1)..(15)

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30 <400> 69
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<210> 70

35 <211> 28

<212> DNA

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<220>

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<222> (1)..(28)

<223>

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<212> DNA

<213> Artificial sequence

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<222> (1)..(31)

<223>

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31

35

<210> 72

<211> 28

<212> DNA

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<213> Artificial sequence

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<400> 72

gtcgacaaca acaacaaaca acctttgc

28

<210> 73

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<211> 28

<212> DNA

10 <213> Artificial sequence

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15

<221> Primer

<222> (1)..(28)

20 <223>

<400> 73

25 ggatccaaca acaacaaaca acctttgc

28

<210> 74

30 <211> 28

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45

<400> 74

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28

5

<210> 75

<211> 28

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<212> DNA

<213> Artificial sequence

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<220>

<221> Primer

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<222> (1)..(28)

<223>

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<400> 75

ctcgagactc actgatttcc attgcttg

28

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<210> 76

<211> 22

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<212> DNA

<213> Artificial sequence

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<220>

<221> Primer

<222> (1)..(22)

<223>

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<400> 76

gagctctaca aattagggtt ac

22

10

<210> 77

<211> 23

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<212> DNA

<213> Artificial sequence

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<220>

<221> Primer

25

<222> (1)..(23)

<223>

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<400> 77

aagcttatta tttccaaatt ccg

23

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<213> Artificial sequence

<220>

<221> Primer

5 <222> (1)..(50)

<223>

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<400> 78

aagctttgca attcatacag aagtgagaaa aatgcagcta gcagcgacag

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15 <210> 79

<211> 1062

<212> DNA

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<213> Haematococcus pluvialis

25 <220>

<221> CDS

<222> (32)..(1021)

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<223>

35 <400> 79

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Met Gln Leu Ala Ala Thr Val

1

5

40 atg ttg gag cag ctt acc gga agc gct gag gca ctc aag gag aag gag

100

Met Leu Glu Gln Leu Thr Gly Ser Ala Glu Ala Leu Lys Glu Lys Glu

10

15

20

aag gag gtt gca ggc agc tct gac gtg ttg cgt aca tgg gcg acc cag

148

45 Lys Glu Val Ala Gly Ser Ser Asp Val Leu Arg Thr Trp Ala Thr Gln

	25		30		35	
	tac tgc ctt ccg tca gag gag tca gac gcg gcc cgc ccg gga ctg aag					196
	Tyr Ser Leu Pro Ser Glu Glu Ser Asp Ala Ala Arg Pro Gly Leu Lys					
5	40		45		50	55
	aat gcc tac aag cca cca cct tcc gac aca aag ggc atc aca atg gcg					244
	Asn Ala Tyr Lys Pro Pro Pro Ser Asp Thr Lys Gly Ile Thr Met Ala					
		60		65		70
10						
	cta gct gtc atc ggc tcc tgg gcc gca gtg ttc ctc cac gcc att ttt					292
	Leu Ala Val Ile Gly Ser Trp Ala Ala Val Phe Leu His Ala Ile Phe					
		75		80		85
	caa atc aag ctt ccg acc tcc ttg gac cag ctg cac tgg ctg ccc gtg					340
15	Gln Ile Lys Leu Pro Thr Ser Leu Asp Gln Leu His Trp Leu Pro Val					
		90		95		100
	tca gat gcc aca gct cag ctg gtt agc ggc agc agc agc ctg ctg cac					388
20	Ser Asp Ala Thr Ala Gln Leu Val Ser Gly Ser Ser Ser Leu Leu His					
		105		110		115
	atc gtc gta gta ttc ttt gtc ctg gag ttc ctg tac aca ggc ctt ttt					436
	Ile Val Val Val Phe Phe Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe					
25	120		125		130	135
	atc acc acg cat gat gct atg cat ggc acc atc gcc atg aga aac agg					484
	Ile Thr Thr His Asp Ala Met His Gly Thr Ile Ala Met Arg Asn Arg					
		140		145		150
30						
	cag ctt aat gac ttc ttg ggc aga gta tgc atc tcc ttg tac gcc tgg					532
	Gln Leu Asn Asp Phe Leu Gly Arg Val Cys Ile Ser Leu Tyr Ala Trp					
		155		160		165
	ttt gat tac aac atg ctg cac cgc aag cat tgg gag cac cac aac cac					580
35	Phe Asp Tyr Asn Met Leu His Arg Lys His Trp Glu His His Asn His					
		170		175		180
	act ggc gag gtg ggc aag gac cct gac ttc cac agg gga aac cct ggc					628
40	Thr Gly Glu Val Gly Lys Asp Pro Asp Phe His Arg Gly Asn Pro Gly					
		185		190		195
	att gtg ccc tgg ttt gcc agc ttc atg tcc agc tac atg tgc atg tgg					676
	Ile Val Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met Ser Met Trp					
45	200		205		210	215

	cag ttt gcg cgc ctc gca tgg tgg acg gtg gtc atg cag ctg ctg ggt	724
	Gln Phe Ala Arg Leu Ala Trp Trp Thr Val Val Met Gln Leu Leu Gly	
	220 225 230	
5	gcg cca atg gcg aac ctg ctg gtg ttc atg gcg gcc gcg ccc atc ctg	772
	Ala Pro Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala Pro Ile Leu	
	235 240 245	
10	tcc gcc ttc cgc ttg ttc tac ttt ggc acg tac atg ccc cac aag cct	820
	Ser Ala Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Met Pro His Lys Pro	
	250 255 260	
	gag cct ggc gcc gcg tca ggc tct tca cca gcc gtc atg aac tgg tgg	868
15	Glu Pro Gly Ala Ala Ser Gly Ser Ser Pro Ala Val Met Asn Trp Trp	
	265 270 275	
	aag tcg cgc act agc cag gcg tcc gac ctg gtc agc ttt ctg acc tgc	916
	Lys Ser Arg Thr Ser Gln Ala Ser Asp Leu Val Ser Phe Leu Thr Cys	
20	280 285 290 295	
	tac cac ttc gac ctg cac tgg gag cac cac cgc tgg ccc ttt gcc ccc	964
	Tyr His Phe Asp Leu His Trp Glu His His Arg Trp Pro Phe Ala Pro	
	300 305 310	
25	tgg tgg gag ctg ccc aac tgc cgc cgc ctg tct ggc cga ggt ctg gtt	1012
	Trp Trp Glu Leu Pro Asn Cys Arg Arg Leu Ser Gly Arg Gly Leu Val	
	315 320 325	
30	cct gcc tag ctggacacac tgcagtgggc cctgctgccca gctgggcatg c	1062
	Pro Ala	
35	<210> 80	
	<211> 329	
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40	<213> Haematococcus pluvialis	
45	<400> 80	

Met Gln, Leu Ala Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala
 1 5 10 15

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 Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val
 20 25 30

10
 Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp
 35 40 45

15
 Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp
 50 55 60

20
 Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp Ala Ala
 65 70 75 80

25
 Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp
 85 90 95

30
 Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser
 100 105 110

35
 Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu Glu
 115 120 125

40
 Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly
 130 135 140

45
 Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val
 145 150 155 160

Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys
 165 170 175

104

His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp
 180 185 190

5 Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met
 195 200 205

10 Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr
 210 215 220

15 Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe
 225 230 235 240

Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly
 245 250 255

20 Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser
 260 265 270

25 Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp
 275 280 285

30 Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His
 290 295 300

35 His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg
 305 310 315 320

Leu Ser Gly Arg Gly Leu Val Pro Ala
 325

40 <210> 81
 <211> 831

<212> DNA

<213> Haematococcus pluvialis

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<220>

<221> CDS

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<222> (1)..(831)

<223>

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<400> 81

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Met Pro Ser Glu Ser Ser Asp Ala Ala Arg Pro Val Leu Lys His Ala

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5

10

15

tat aaa cct cca gca tct gac gcc aag ggc atc act atg gcg ctg acc 96

Tyr Lys Pro Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr

20

25

30

25

atc att ggc acc tgg acc gca gtg ttt tta cac gca ata ttc caa atc 144

Ile Ile Gly Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile

35

40

45

30

agg cta ccg aca tcc atg gac cag ctt cac tgg ttg cct gtg tcc gaa 192

Arg Leu Pro Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu

50

55

60

gcc aca gcc cag ctg ttg ggc gga agc agc agc cta ttg cac atc gcc 240

35

Ala Thr Ala Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala

65

70

75

80

gca gtc ttc att gta ctt gag ttt ctg tac act ggt cta ttc atc acc 288

Ala Val Phe Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr

40

85

90

95

acg cat gat gca atg cat ggc acc ata gct ttg agg aac agg cag ctc 336

Thr His Asp Ala Met His Gly Thr Ile Ala Leu Arg Asn Arg Gln Leu

100

105

110

45

106

	aat gat ctc ctt ggc aac atc tgc ata tca ctg tac gcc tgg ttt gac	384
	Asn Asp Leu Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp	
	115 120 125	
5	tac agc atg cac tgg gag cac cac aac cat act ggc gaa gtg ggg aaa	432
	Tyr Ser Met His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys	
	130 135 140	
10	gac cct gac ttc cac aaa gga aat cct ggc ctt gtc ccc tgg ttc gcc	480
	Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val Pro Trp Phe Ala	
	145 150 155 160	
15	agc ttc atg tcc agc tac atg tcc ctg tgg cag ttt gcc cgg ctg gca	528
	Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe Ala Arg Leu Ala	
	165 170 175	
20	tgg tgg gca gtg gtg atg caa acg ttg ggg gcc ccc atg gcg aat ctc	576
	Trp Trp Ala Val Val Met Gln Thr Leu Gly Ala Pro Met Ala Asn Leu	
	180 185 190	
25	cta gtc ttc atg gct gca gcc cca atc ttg tca gca ttc cgc ctc ttc	624
	Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe	
	195 200 205	
30	ggc tct cag gtc atg tct tgg ttc agg gcc aag aca agt gag gca tct	720
	Gly Ser Gln Val Met Ser Trp Phe Arg Ala Lys Thr Ser Glu Ala Ser	
	225 230 235 240	
35	gat gtg atg agc ttc ctg aca tgc tac cac ttt gac ctg ttt gcc ccc	768
	Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu Phe Ala Pro	
	245 250 255	
40	tgg tgg cag ctg ccc cac tgc cgc cgc ctg tct ggg cgt ggc ctg gtg	816
	Trp Trp Gln Leu Pro His Cys Arg Arg Leu Ser Gly Arg Gly Leu Val	
	260 265 270	
45	cct gcc ttg gca tga	831
	Pro Ala Leu Ala	
	275	

<210> 82

<211> 276

5 <212> PRT

<213> Haematococcus pluvialis

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<400> 82

Met Pro Ser Glu Ser Ser Asp Ala Ala Arg Pro Val Leu Lys His Ala
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Tyr Lys Pro Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr
 20 25 30

20

Ile Ile Gly Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile
 35 40 45

25

Arg Leu Pro Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu
 50 55 60

30

Ala Thr Ala Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala
 65 70 75 80

35

Ala Val Phe Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr
 85 90 95

40

Thr His Asp Ala Met His Gly Thr Ile Ala Leu Arg Asn Arg Gln Leu
 100 105 110

Asn Asp Leu Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp
 115 120 125

45

Tyr Ser Met His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys

130

135

140

5 Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val Pro Trp Phe Ala
145 150 155 160

10 Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe Ala Arg Leu Ala
165 170 175

15 Trp Trp Ala Val Val Met Gln Thr Leu Gly Ala Pro Met Ala Asn Leu
180 185 190

20 Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe
195 200 205

25 Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro Gly Pro Ala Ala
210 215 220

30 Gly Ser Gln Val Met Ser Trp Phe Arg Ala Lys Thr Ser Glu Ala Ser
225 230 235 240

35 Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu Phe Ala Pro
245 250 255

40 Trp Trp Gln Leu Pro His Cys Arg Arg Leu Ser Gly Arg Gly Leu Val
260 265 270

45 Pro Ala Leu Ala
275

<210> 83

<211> 729

<212> DNA

<213> Paracoccus sp. MBIC1143

5 <220>

<221> CDS

<222> (1)..(729)

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<223>

15 <400> 83

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 Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
 1 5 10 15

20 atc gtc tcg ggc ggc atc atc gcc gct tgg ctg gcc ctg cat gtg cat 96
 Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
 20 25 30

25 gcg ctg tgg ttt ctg gac gca gcg gcg cat ccc atc ctg gcg atc gca 144
 Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala
 35 40 45

30 aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg 192
 Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
 50 55 60

cat gac gcg atg cac ggg tcg gtg gtg ccg ggg cgt ccg cgc gcc aat 240
 His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
 65 70 75 80

35 gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg 288
 Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
 85 90 95

40 cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc 336
 Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
 100 105 110

45 gac gac gac ccc gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc 384
 Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala

110

	115	120	125	
	cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc			432
	Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro			
5	130	135	140	
	gtc atc gtg acg gtc tat gcg ctg atc ctt ggg gat cgc tgg atg tac			480
	Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr			
	145	150	155	160
10				
	gtg gtc ttc tgg ccg ctg ccg tcg atc ctg gcg tcg atc cag ctg ttc			528
	Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe			
	165	170	175	
15	gtg ttc ggc acc tgg ctg ccg cac cgc ccc ggc cac gac gcg ttc ccg			576
	Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro			
	180	185	190	
	gac cgc cac aat gcg cgg tcg tcg cgg atc agc gac ccc gtg tcg ctg			624
20	Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu			
	195	200	205	
	ctg acc tgc ttt cac ttt ggc ggt tat cat cac gaa cac cac ctg cac			672
	Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His			
25	210	215	220	
	ccg acg gtg ccg tgg tgg cgc ctg ccc agc acc cgc acc aag ggg gac			720
	Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp			
	225	230	235	240
30				
	acc gca tga			729
	Thr Ala			
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	<210> 84			
	<211> 242			
40	<212> PRT			
	<213> Paracoccus sp. MBIC1143			
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<400> 84

Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
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 Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
 20 25 30
 10
 Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala
 35 40 45
 15
 Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
 50 55 60
 20
 His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
 65 70 75 80
 Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
 85 90 95
 25
 Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
 100 105 110
 30
 Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
 115 120 125
 35
 Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
 130 135 140
 Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
 145 150 155 160
 40
 Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
 165 170 175
 45

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
 180 185 190

5

Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
 195 200 205

10

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
 210 215 220

15

Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp
 225 230 235 240

Thr Ala

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<210> 85

<211> 735

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<212> DNA

<213> Brevundimonas aurantiaca

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<220>

<221> CDS

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<222> (1) .. (735)

<223>

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<400> 85

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 Met Thr Ala Ala Val Ala Glu Pro Arg Thr Val Pro Arg Gln Thr Trp

48

45

1 5 10 15

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5	cat gtc tac ggc gtc tat ttt cac cga tgg ggg ccg ttg acc ctg gtg His Val Tyr Gly Val Tyr Phe His Arg Trp Gly Pro Leu Thr Leu Val 35 40 45	144
10	atc gcc ccg gcg atc gtg gcg gtc cag acc tgg ttg tcg gtc ggc ctt Ile Ala Pro Ala Ile Val Ala Val Gln Thr Trp Leu Ser Val Gly Leu 50 55 60	192
15	ttc atc gtc gcc cat gac gcc atg tac ggc tcc ctg gcg ccg gga cgg Phe Ile Val Ala His Asp Ala Met Tyr Gly Ser Leu Ala Pro Gly Arg 65 70 75 80	240
20	ccg cgg ctg aac gcc gca gtc ggc cgg ctg acc ctg ggg ctc tat gcg Pro Arg Leu Asn Ala Ala Val Gly Arg Leu Thr Leu Gly Leu Tyr Ala 85 90 95	288
25	ggc ttc cgc ttc gat cgg ctg aag acg gcg cac cac gcc cac cac gcc Gly Phe Arg Phe Asp Arg Leu Lys Thr Ala His His Ala His His Ala 100 105 110	336
30	gcg ccc ggc acg gcc gac gac ccg gat ttt cac gcc ccg gcg ccc cgc Ala Pro Gly Thr Ala Asp Asp Pro Asp Phe His Ala Pro Ala Pro Arg 115 120 125	384
35	gcc ttc ctt ccc tgg ttc ctg aac ttc ttt cgc acc tat ttc ggc tgg Ala Phe Leu Pro Trp Phe Leu Asn Phe Phe Arg Thr Tyr Phe Gly Trp 130 135 140	432
40	cgc gag atg gcg gtc ctg acc gcc ctg gtc ctg atc gcc ctc ttc ggc Arg Glu Met Ala Val Leu Thr Ala Leu Val Leu Ile Ala Leu Phe Gly 145 150 155 160	480
45	ctg ggg gcg cgg ccg gcc aat ctc ctg acc ttc tgg gcc gcg ccg gcc Leu Gly Ala Arg Pro Ala Asn Leu Leu Thr Phe Trp Ala Ala Pro Ala 165 170 175	528
	ctg ctt tca gcg ctt cag ctc ttc acc ttc ggc acc tgg ctg ccg cac Leu Leu Ser Ala Leu Gln Leu Phe Thr Phe Gly Thr Trp Leu Pro His 180 185 190	576

114

cgc cac acc gac cag ccg ttc gcc gac ggc cac cac gcc cgc agc agc 624
 Arg His Thr Asp Gln Pro Phe Ala Asp Ala His His Ala Arg Ser Ser
 195 200 205

5 ggc tac ggc ccc gtg ctt tcc ctg ctc acc tgt ttc cac ttc ggc cgc 672
 Gly Tyr Gly Pro Val Leu Ser Leu Leu Thr Cys Phe His Phe Gly Arg
 210 215 220

10 cac cac gaa cac cat ctg agc ccc tgg cgg ccc tgg tgg cgt ctg tgg 720
 His His Glu His His Leu Ser Pro Trp Arg Pro Trp Trp Arg Leu Trp
 225 230 235 240

15 cgc ggc gag tct tga 735
 Arg Gly Glu Ser

<210> 86

20 <211> 244
 <212> PRT
 <213> Brevundimonas aurantiaca

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<400> 86

30 Met Thr Ala Ala Val Ala Glu Pro Arg Thr Val Pro Arg Gln Thr Trp
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35 Ile Gly Leu Thr Leu Ala Gly Met Ile Val Ala Gly Trp Ala Val Leu
 20 25 30

40 His Val Tyr Gly Val Tyr Phe His Arg Trp Gly Pro Leu Thr Leu Val
 35 40 45

45 Ile Ala Pro Ala Ile Val Ala Val Gln Thr Trp Leu Ser Val Gly Leu
 50 55 60

115

Phe Ile Val Ala His Asp Ala Met Tyr Gly Ser Leu Ala Pro Gly Arg
 65 70 75 80

5 Pro Arg Leu Asn Ala Ala Val Gly Arg Leu Thr Leu Gly Leu Tyr Ala
 85 90 95

10 Gly Phe Arg Phe Asp Arg Leu Lys Thr Ala His His Ala His His Ala
 100 105 110

15 Ala Pro Gly Thr Ala Asp Asp Pro Asp Phe His Ala Pro Ala Pro Arg
 115 120 125

Ala Phe Leu Pro Trp Phe Leu Asn Phe Phe Arg Thr Tyr Phe Gly Trp
 130 135 140

20 Arg Glu Met Ala Val Leu Thr Ala Leu Val Leu Ile Ala Leu Phe Gly
 145 150 155 160

25 Leu Gly Ala Arg Pro Ala Asn Leu Leu Thr Phe Trp Ala Ala Pro Ala
 165 170 175

30 Leu Leu Ser Ala Leu Gln Leu Phe Thr Phe Gly Thr Trp Leu Pro His
 180 185 190

35 Arg His Thr Asp Gln Pro Phe Ala Asp Ala His His Ala Arg Ser Ser
 195 200 205

Gly Tyr Gly Pro Val Leu Ser Leu Leu Thr Cys Phe His Phe Gly Arg
 210 215 220

40 His His Glu His His Leu Ser Pro Trp Arg Pro Trp Trp Arg Leu Trp
 225 230 235 240

45 Arg Gly Glu Ser

5 <210> 87
 <211> 690
 <212> DNA
 10 <213> Nodularia spumigena NSOR10
 15 <220>
 <221> CDS
 <222> (1)..(690)
 20 <223>
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 Met Ala Ile Ala Ile Ile Ser Ile Trp Ala Ile Ser Leu Gly Leu Leu
 1 5 10 15
 30 ctt tat att gat ata tcc caa ttc aag ttt tgg atg ttg tta ccg ctc 96
 Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp Met Leu Leu Pro Leu
 20 25 30
 35 ata ttt tgg caa aca ttt tta tat acg gga tta ttt att aca gct cat 144
 Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
 35 40 45
 gat gcc atg cat ggg gta gtt ttt ccc aaa aat ccc aaa atc aac cat 192
 Asp Ala Met His Gly Val Val Phe Pro Lys Asn Pro Lys Ile Asn His
 50 55 60
 40 ttc att ggc tca ttg tgc ctg ttt ctt tat ggt ctt tta cct tat caa 240
 Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly Leu Leu Pro Tyr Gln
 65 70 75 80
 45 aaa ctt tta aaa aag cat tgg cta cat cac cat aat cca gcc agt gaa 288

<212> PRT

<213> Nodularia spumigena NSOR10

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<400> 88

Met Ala Ile Ala Ile Ile Ser Ile Trp Ala Ile Ser Leu Gly Leu Leu
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Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp Met Leu Leu Pro Leu
 20 25 30

15

Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
 35 40 45

20

Asp Ala Met His Gly Val Val Phe Pro Lys Asn Pro Lys Ile Asn His
 50 55 60

Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly Leu Leu Pro Tyr Gln
 65 70 75 80

Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser Glu
 85 90 95

30

Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys Asn Phe Phe Ala Trp
 100 105 110

35

Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp Leu Gln Ile Ile Thr
 115 120 125

40

Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile Trp His Phe Pro Glu
 130 135 140

Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser Ile Leu Ser Ser Leu

45

119

145 150 155 160
 Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Val Glu
 5 165 170 175
 Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile Ser Arg Pro Ile Trp
 10 180 185 190
 Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Tyr Glu His His
 15 195 200 205
 Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Glu Ile Tyr Lys Met
 210 215 220
 20 Ser Lys Ser Asn Leu
 225
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 25 <211> 789
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	Leu	Ser	Ala	Lys	Glu	Asp	Thr	Val	Trp	Gly	Leu	Val	Ile	Val	Ile	Val	
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10	att	att	agt	ctt	tgg	gta	gct	agt	ttg	gct	ttt	tta	cta	gct	att	aat	144
	Ile	Ile	Ser	Leu	Trp	Val	Ala	Ser	Leu	Ala	Phe	Leu	Leu	Ala	Ile	Asn	
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	Tyr	Ala	Lys	Val	Pro	Ile	Trp	Leu	Ile	Pro	Ile	Ala	Ile	Val	Trp	Gln	
		50					55					60					
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	Met	Phe	Leu	Tyr	Thr	Gly	Leu	Phe	Ile	Thr	Ala	His	Asp	Ala	Met	His	
	65					70				75				80			
25	ggg	tca	gtt	tat	cgt	aaa	aat	ccc	aaa	att	aat	aat	ttt	atc	ggg	tca	288
	Gly	Ser	Val	Tyr	Arg	Lys	Asn	Pro	Lys	Ile	Asn	Asn	Phe	Ile	Gly	Ser	
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	Leu	Ala	Val	Ala	Leu	Tyr	Ala	Val	Phe	Pro	Tyr	Gln	Gln	Met	Leu	Lys	
				100					105					110			
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	Asn	His	Cys	Leu	His	His	Arg	His	Pro	Ala	Ser	Glu	Val	Asp	Pro	Asp	
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	Phe	His	Asp	Gly	Lys	Arg	Thr	Asn	Ala	Ile	Phe	Trp	Tyr	Leu	His	Phe	
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	Met	Ile	Glu	Tyr	Ser	Ser	Trp	Gln	Gln	Leu	Ile	Val	Leu	Thr	Ile	Leu	
	145					150				155					160		
50	ttt	aat	tta	gct	aaa	tac	gtt	ttg	cac	atc	cat	caa	ata	aat	ctc	atc	528
	Phe	Asn	Leu	Ala	Lys	Tyr	Val	Leu	His	Ile	His	Gln	Ile	Asn	Leu	Ile	
					165				170					175			
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121

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	Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr			
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	ccc cat tgc agc caa aca ata aaa ttg cca act ttt ttg tca ttt atc			672
	Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile			
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	Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His			
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	gta cct tgg tgg caa ctt cca tct gta tat aag cag aga gta ttc aac			768
	Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn			
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	20	25	30	
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	Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn			
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Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln
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Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His
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Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser
 85 90 95

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Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys
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Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp
 115 120 125

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Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe
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Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu
 145 150 155 160

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Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile
 165 170 175

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Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr
 180 185 190

Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr
 195 200 205

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Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile
 210 215 220

123

Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
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40 gta ctg aga agt aaa tct cag ttt aag ggg ctt ttc att gct att gtc 96
 Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val
 20 25 30

45 att gtt agc gca tgg gtc att agc ctg agt tta tta ctt tcc ctt gac 144
 Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Ser Leu Asp
 35 40 45

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	50 55 60	
5	aca ttt tta tat acg gga tta ttt att aca tct cat gat gcc atg cat	240
	Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His	
	65 70 75 80	
10	ggc gta gta ttt ccc caa aac acc aag att aat cat ttg att gga aca	288
	Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr	
	85 90 95	
15	ttg acc cta tcc ctt tat ggt ctt tta cca tat caa aaa cta ttg aaa	336
	Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys	
	100 105 110	
20	aaa cat tgg tta cac cac cac aat cca gca agc tca ata gac ccg gat	384
	Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp	
	115 120 125	
25	ttt cac aat ggt aaa cac caa agt ttc ttt gct tgg tat ttt cat ttt	432
	Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe	
	130 135 140	
30	atg aaa ggt tac tgg agt tgg ggg caa ata att gcg ttg act att att	480
	Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile	
	145 150 155 160	
35	tat aac ttt gct aaa tac ata ctc cat atc cca agt gat aat cta act	528
	Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr	
	165 170 175	
40	tac ttt tgg gtg cta ccc tcg ctt tta agt tca tta caa tta ttc tat	576
	Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr	
	180 185 190	
45	ttt ggt act ttt tta ccc cat agt gaa cca ata ggg ggt tat gtt cag	624
	Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln	
	195 200 205	
50	cct cat tgt gcc caa aca att agc cgt cct att tgg tgg tca ttt atc	672
	Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile	
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 Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
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30 Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Ser Leu Asp
 35 40 45

35 Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln
 50 55 60

40 Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His
 65 70 75 80

Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr
 85 90 95

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Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys
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5 Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp
 115 120 125

10 Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe
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Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr
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20 Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr
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25 Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln
 195 200 205

30 Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile
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gtg	act	gct	gcc	tac	gcc	gcc	cgg	gcg	ggc	ctg	aaa	gtc	ggc	gtg	ttc	96
Val	Thr	Ala	Ala	Tyr	Ala	Ala	Arg	Ala	Gly	Leu	Lys	Val	Gly	Val	Phe	
			20				25					30				

25

gag	cgg	cgg	cac	ctc	gtc	ggc	ggg	gcg	gtc	agc	acc	gag	gag	gtc	gtg	144
Glu	Arg	Arg	His	Leu	Val	Gly	Gly	Ala	Val	Ser	Thr	Glu	Glu	Val	Val	
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ccc	ggt	tac	cgc	ttc	gac	tac	ggc	ggc	agc	gcc	cac	atc	ctg	att	cgg	192
Pro	Gly	Tyr	Arg	Phe	Asp	Tyr	Gly	Gly	Ser	Ala	His	Ile	Leu	Ile	Arg	
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atg	acg	ccc	atc	gtg	cgc	gaa	ctc	gaa	ctc	acg	cgg	cac	ggg	ctg	cat	240
Met	Thr	Pro	Ile	Val	Arg	Glu	Leu	Glu	Leu	Thr	Arg	His	Gly	Leu	His	
	65				70					75				80		

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tac	ctc	gaa	gtg	gac	cct	atg	ttt	cac	gct	tcc	gac	ggc	gaa	acg	ccc	288
Tyr	Leu	Glu	Val	Asp	Pro	Met	Phe	His	Ala	Ser	Asp	Gly	Glu	Thr	Pro	
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Trp	Phe	Ile	His	Arg	Asp	Ala	Gly	Arg	Thr	Ile	Arg	Glu	Leu	Asp	Glu	
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	Thr Pro Phe Ala Arg Ala Val Ala Asp Leu Phe Asn Ser Ala Pro Gly	
	130 135 140	
10	ccg ctc gac ctg ggc aaa atg gtg atg cgc agc ggc cag ggc aag gac	480
	Pro Leu Asp Leu Gly Lys Met Val Met Arg Ser Gly Gln Gly Lys Asp	
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	Trp Asn Glu Gln Leu Pro Arg Ile Leu Arg Pro Tyr Gly Asp Val Ala	
	165 170 175	
20	cgc gag tac ttc agc gag gag cgc gtg cgg gct ccc ctg acc tgg atg	576
	Arg Glu Tyr Phe Ser Glu Glu Arg Val Arg Ala Pro Leu Thr Trp Met	
	180 185 190	
	gcg gcc cag agc ggc ccc cca ccc tcg gac ccg ctg agc gcg ccc ttt	624
	Ala Ala Gln Ser Gly Pro Pro Pro Ser Asp Pro Leu Ser Ala Pro Phe	
	195 200 205	
25	ttg ctg tgg cac ccg ctc tac cac gaa ggc ggc gtg gcg cgg ccc aaa	672
	Leu Leu Trp His Pro Leu Tyr His Glu Gly Gly Val Ala Arg Pro Lys	
	210 215 220	
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	Gly Gly Ser Gly Gly Leu Thr Lys Ala Leu Arg Arg Ala Thr Glu Ala	
	225 230 235 240	
35	gaa ggc ggc gag gtc ttc acc gac gcg ccg gtc aag gaa att ctg gtc	768
	Glu Gly Gly Glu Val Phe Thr Asp Ala Pro Val Lys Glu Ile Leu Val	
	245 250 255	
40	aag gac ggc aag gcg cag ggc atc cgg ctg gaa agc ggc gag acg tac	816
	Lys Asp Gly Lys Ala Gln Gly Ile Arg Leu Glu Ser Gly Glu Thr Tyr	
	260 265 270	
	acc gcc cgc gcc gtc gtg tcg ggc gtc cac atc ctg acc act gcg aat	864
	Thr Ala Arg Ala Val Val Ser Gly Val His Ile Leu Thr Thr Ala Asn	
	275 280 285	
45	gcc ctg ccc gcc gaa tat gtc cct agc gcc gcc agg aat gtg cgc gtg	912

129

	Ala	Leu	Pro	Ala	Glu	Tyr	Val	Pro	Ser	Ala	Ala	Arg	Asn	Val	Arg	Val	
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	Gly	Asn	Gly	Phe	Gly	Met	Ile	Leu	Arg	Leu	Ala	Leu	Ser	Glu	Lys	Val	
	305				310					315					320		
10	aaa	tac	cgt	cac	cac	acc	gag	ccc	gac	tca	cgc	atc	ggc	ctg	gga	ttg	1008
	Lys	Tyr	Arg	His	His	Thr	Glu	Pro	Asp	Ser	Arg	Ile	Gly	Leu	Gly	Leu	
				325					330					335			
15	ctg	atc	aaa	aac	gag	cgg	caa	atc	atg	cag	ggc	tac	ggc	gaa	tac	ctc	1056
	Leu	Ile	Lys	Asn	Glu	Arg	Gln	Ile	Met	Gln	Gly	Tyr	Gly	Glu	Tyr	Leu	
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	Ala	Gly	Gln	Pro	Thr	Thr	Asp	Pro	Pro	Leu	Val	Ala	Met	Ser	Phe	Ser	
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25	gcg	gtg	gac	gac	tcg	ctc	gcc	cca	ccg	aac	ggc	gac	gtg	ttg	tgg	ctg	1152
	Ala	Val	Asp	Asp	Ser	Leu	Ala	Pro	Pro	Asn	Gly	Asp	Val	Leu	Trp	Leu	
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	Trp	Ala	Gln	Tyr	Tyr	Pro	Phe	Glu	Leu	Ala	Thr	Gly	Ser	Trp	Glu	Thr	
	385				390					395				400			
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	Arg	Thr	Ala	Glu	Ala	Arg	Glu	Asn	Ile	Leu	Arg	Ala	Phe	Glu	His	Tyr	
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	Ala	Pro	Gly	Thr	Arg	Asp	Thr	Ile	Val	Gly	Glu	Leu	Val	Gln	Thr	Pro	
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	Gln	Trp	Leu	Glu	Thr	Asn	Leu	Gly	Leu	His	Arg	Gly	Asn	Val	Met	His	
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	Leu	Glu	Met	Ser	Phe	Asp	Gln	Met	Phe	Ser	Phe	Arg	Pro	Trp	Leu	Lys	
	450					455					460						
55	gcg	agc	cag	tac	cgc	tgg	ccg	ggc	gtg	cag	ggg	ctg	tac	ctc	acc	ggc	1440
	Ala	Ser	Gln	Tyr	Arg	Trp	Pro	Gly	Val	Gln	Gly	Leu	Tyr	Leu	Thr	Gly	

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 Pro Gly Tyr Arg Phe Asp Tyr Gly Gly Ser Ala His Ile Leu Ile Arg
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 65 70 75 80
 Tyr Leu Glu Val Asp Pro Met Phe His Ala Ser Asp Gly Glu Thr Pro
 45 85 90 95

131

Trp Phe Ile His Arg Asp Ala Gly Arg Thr Ile Arg Glu Leu Asp Glu
 100 105 110
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 Lys Phe Pro Gly Gln Gly Asp Ala Tyr Gly Arg Phe Leu Asp Asp Trp
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 Thr Pro Phe Ala Arg Ala Val Ala Asp Leu Phe Asn Ser Ala Pro Gly
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 Pro Leu Asp Leu Gly Lys Met Val Met Arg Ser Gly Gln Gly Lys Asp
 145 150 155 160
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 Glu Gly Gly Glu Val Phe Thr Asp Ala Pro Val Lys Glu Ile Leu Val
 245 250 255
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 Lys Asp Gly Lys Ala Gln Gly Ile Arg Leu Glu Ser Gly Glu Thr Tyr
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Thr Ala Arg Ala Val Val Ser Gly Val His Ile Leu Thr Thr Ala Asn
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Ala Leu Pro Ala Glu Tyr Val Pro Ser Ala Ala Arg Asn Val Arg Val
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Gly Asn Gly Phe Gly Met Ile Leu Arg Leu Ala Leu Ser Glu Lys Val
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Lys Tyr Arg His His Thr Glu Pro Asp Ser Arg Ile Gly Leu Gly Leu
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Leu Ile Lys Asn Glu Arg Gln Ile Met Gln Gly Tyr Gly Glu Tyr Leu
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Ala Gly Gln Pro Thr Thr Asp Pro Pro Leu Val Ala Met Ser Phe Ser
 355 360 365

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Ala Val Asp Asp Ser Leu Ala Pro Pro Asn Gly Asp Val Leu Trp Leu
 370 375 380

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Trp Ala Gln Tyr Tyr Pro Phe Glu Leu Ala Thr Gly Ser Trp Glu Thr
 385 390 395 400

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Arg Thr Ala Glu Ala Arg Glu Asn Ile Leu Arg Ala Phe Glu His Tyr
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Ala Pro Gly Thr Arg Asp Thr Ile Val Gly Glu Leu Val Gln Thr Pro
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Gln Trp Leu Glu Thr Asn Leu Gly Leu His Arg Gly Asn Val Met His
 435 440 445

133

Leu Glu Met Ser Phe Asp Gln Met Phe Ser Phe Arg Pro Trp Leu Lys
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5 Ala Ser Gln Tyr Arg Trp Pro Gly Val Gln Gly Leu Tyr Leu Thr Gly
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<212> DNA

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134

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5	aaa ctt ttt tgt agc ttt ctt gat tta gca ccc aca tca aag cca gag	192
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	Ser Leu Asp Val Asn Ile Ser Trp Val Asp Pro Asn Ser Asn Arg Ala	
	65 70 75 80	
15	caa ttc gac gtg atc att atc gga gct ggc cct gct ggg ctc agg cta	288
	Gln Phe Asp Val Ile Ile Ile Gly Ala Gly Pro Ala Gly Leu Arg Leu	
	85 90 95	
20	gct gaa caa gtt tct aaa tat ggt att aag gta tgt tgt gtt gac cct	336
	Ala Glu Gln Val Ser Lys Tyr Gly Ile Lys Val Cys Cys Val Asp Pro	
	100 105 110	
25	tca cca ctc tcc atg tgg cca aat aat tat ggt gtt tgg gtt gat gag	384
	Ser Pro Leu Ser Met Trp Pro Asn Asn Tyr Gly Val Trp Val Asp Glu	
	115 120 125	
30	ttt gag aat tta gga ctg gaa aat tgt tta gat cat aaa tgg cct atg	432
	Phe Glu Asn Leu Gly Leu Glu Asn Cys Leu Asp His Lys Trp Pro Met	
	130 135 140	
35	act tgt gtg cat ata aat gat aac aaa act aag tat ttg gga aga cca	480
	Thr Cys Val His Ile Asn Asp Asn Lys Thr Lys Tyr Leu Gly Arg Pro	
	145 150 155 160	
40	tat ggt aga gtt agt aga aag aag ctg aag ttg aaa ttg ttg aat agt	528
	Tyr Gly Arg Val Ser Arg Lys Lys Leu Lys Leu Lys Leu Leu Asn Ser	
	165 170 175	
45	tgt gtt gag aac aga gtg aag ttt tat aaa gct aag gtt tgg aaa gtg	576
	Cys Val Glu Asn Arg Val Lys Phe Tyr Lys Ala Lys Val Trp Lys Val	
	180 185 190	
50	gaa cat gaa gaa ttt gag tct tca att gtt tgt gat gat ggt aag aag	624
	Glu His Glu Glu Phe Glu Ser Ser Ile Val Cys Asp Asp Gly Lys Lys	
	195 200 205	
55	ata aga ggt agt ttg gtt gtg gat gca agt ggt ttt gct agt gat ttt	672

135

	Ile	Arg	Gly	Ser	Leu	Val	Val	Asp	Ala	Ser	Gly	Phe	Ala	Ser	Asp	Phe	
	210						215					220					
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5	Ile	Glu	Tyr	Asp	Arg	Pro	Arg	Asn	His	Gly	Tyr	Gln	Ile	Ala	His	Gly	
	225					230				235						240	
	gtt	tta	gta	gaa	gtt	gat	aat	cat	cca	ttt	gat	ttg	gat	aaa	atg	gtg	768
10	Val	Leu	Val	Glu	Val	Asp	Asn	His	Pro	Phe	Asp	Leu	Asp	Lys	Met	Val	
					245					250					255		
	ctt	atg	gat	tgg	agg	gat	tct	cat	ttg	ggg	aat	gag	cca	tat	tta	agg	816
	Leu	Met	Asp	Trp	Arg	Asp	Ser	His	Leu	Gly	Asn	Glu	Pro	Tyr	Leu	Arg	
				260					265					270			
15	gtg	aat	aat	gct	aaa	gaa	cca	aca	ttc	ttg	tat	gca	atg	cca	ttt	gat	864
	Val	Asn	Asn	Ala	Lys	Glu	Pro	Thr	Phe	Leu	Tyr	Ala	Met	Pro	Phe	Asp	
		275						280					285				
20	aga	gat	ttg	gtt	ttc	ttg	gaa	gag	act	tct	ttg	gtg	agt	cgt	cct	gtt	912
	Arg	Asp	Leu	Val	Phe	Leu	Glu	Glu	Thr	Ser	Leu	Val	Ser	Arg	Pro	Val	
		290					295					300					
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25	Leu	Ser	Tyr	Met	Glu	Val	Lys	Arg	Arg	Met	Val	Ala	Arg	Leu	Arg	His	
	305					310					315				320		
	ttg	ggg	atc	aaa	gtg	aaa	agt	gtt	att	gag	gaa	gag	aaa	tgt	gtg	atc	1008
30	Leu	Gly	Ile	Lys	Val	Lys	Ser	Val	Ile	Glu	Glu	Glu	Lys	Cys	Val	Ile	
				325					330					335			
	cct	atg	gga	gga	cca	ctt	ccg	cgg	att	cct	caa	aat	gtt	atg	gct	att	1056
	Pro	Met	Gly	Gly	Pro	Leu	Pro	Arg	Ile	Pro	Gln	Asn	Val	Met	Ala	Ile	
				340					345					350			
35	ggg	ggg	aat	tca	ggg	ata	gtt	cat	cca	tca	aca	ggg	tac	atg	gtg	gct	1104
	Gly	Gly	Asn	Ser	Gly	Ile	Val	His	Pro	Ser	Thr	Gly	Tyr	Met	Val	Ala	
		355						360					365				
40	agg	agc	atg	gct	tta	gca	cca	gta	cta	gct	gaa	gcc	atc	gtc	gag	ggg	1152
	Arg	Ser	Met	Ala	Leu	Ala	Pro	Val	Leu	Ala	Glu	Ala	Ile	Val	Glu	Gly	
		370					375					380					
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45	Leu	Gly	Ser	Thr	Arg	Met	Ile	Arg	Gly	Ser	Gln	Leu	Tyr	His	Arg	Val	

136

	385	390	395	400	
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	Trp Asn Gly Leu Trp Pro Leu Asp Arg Arg Cys Val Arg Glu Cys Tyr				
5		405	410	415	
	tca ttt ggg atg gag aca ttg ttg aag ctt gat ttg aaa ggg act agg				1296
	Ser Phe Gly Met Glu Thr Leu Leu Lys Leu Asp Leu Lys Gly Thr Arg				
		420	425	430	
10					
	aga ttg ttt gac gct ttc ttt gat ctt gat cct aaa tac tgg caa ggg				1344
	Arg Leu Phe Asp Ala Phe Phe Asp Leu Asp Pro Lys Tyr Trp Gln Gly				
		435	440	445	
15					
	ttc ctt tct tca aga ttg tct gtc aaa gaa ctt ggt tta ctc agc ttg				1392
	Phe Leu Ser Ser Arg Leu Ser Val Lys Glu Leu Gly Leu Leu Ser Leu				
		450	455	460	
	tgt ctt ttc gga cat ggc tca aac atg act agg ttg gat att gtt aca				1440
20	Cys Leu Phe Gly His Gly Ser Asn Met Thr Arg Leu Asp Ile Val Thr				
		465	470	475	480
	aaa tgt cct ctt cct ttg gtt aga ctg att ggc aat cta gca ata gag				1488
	Lys Cys Pro Leu Pro Leu Val Arg Leu Ile Gly Asn Leu Ala Ile Glu				
25		485	490	495	
	agc ctt tgaatgtgaa aagtttgaat cattttcttc attttaattt ctttgattat				1544
	Ser Leu				
30					
	tttcatatatt tctcaattgc aaaagtgaga taagagctac atactgtcaa caaataaact				1604
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40 <211> 498

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45 <213> Lycopersicon esculentum

<400> 96.

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15 Thr Thr Lys Lys Lys Ser Arg Lys Cys Leu Leu Arg Asn Lys Ser Ser
 35 40 45

20 Lys Leu Phe Cys Ser Phe Leu Asp Leu Ala Pro Thr Ser Lys Pro Glu
 50 55 60

25 Ser Leu Asp Val Asn Ile Ser Trp Val Asp Pro Asn Ser Asn Arg Ala
 65 70 75 80

30 Gln Phe Asp Val Ile Ile Ile Gly Ala Gly Pro Ala Gly Leu Arg Leu
 85 90 95

35 Ala Glu Gln Val Ser Lys Tyr Gly Ile Lys Val Cys Cys Val Asp Pro
 100 105 110

40 Ser Pro Leu Ser Met Trp Pro Asn Asn Tyr Gly Val Trp Val Asp Glu
 115 120 125

45 Phe Glu Asn Leu Gly Leu Glu Asn Cys Leu Asp His Lys Trp Pro Met
 130 135 140

50 Thr Cys Val His Ile Asn Asp Asn Lys Thr Lys Tyr Leu Gly Arg Pro
 145 150 155 160

55 Tyr Gly Arg Val Ser Arg Lys Lys Leu Lys Leu Lys Leu Asn Ser

138

165

170

175

5 Cys Val Glu Asn Arg Val Lys Phe Tyr Lys Ala Lys Val Trp Lys Val
180 185 190

10 Glu His Glu Glu Phe Glu Ser Ser Ile Val Cys Asp Asp Gly Lys Lys
195 200 205

15 Ile Arg Gly Ser Leu Val Val Asp Ala Ser Gly Phe Ala Ser Asp Phe
210 215 220

Ile Glu Tyr Asp Arg Pro Arg Asn His Gly Tyr Gln Ile Ala His Gly
225 230 235 240

20 Val Leu Val Glu Val Asp Asn His Pro Phe Asp Leu Asp Lys Met Val
245 250 255

25 Leu Met Asp Trp Arg Asp Ser His Leu Gly Asn Glu Pro Tyr Leu Arg
260 265 270

30 Val Asn Asn Ala Lys Glu Pro Thr Phe Leu Tyr Ala Met Pro Phe Asp
275 280 285

Arg Asp Leu Val Phe Leu Glu Glu Thr Ser Leu Val Ser Arg Pro Val
290 295 300

35 Leu Ser Tyr Met Glu Val Lys Arg Arg Met Val Ala Arg Leu Arg His
305 310 315 320

40 Leu Gly Ile Lys Val Lys Ser Val Ile Glu Glu Glu Lys Cys Val Ile
325 330 335

45 Pro Met Gly Gly Pro Leu Pro Arg Ile Pro Gln Asn Val Met Ala Ile
340 345 350

Gly Gly Asn Ser Gly Ile Val His Pro Ser Thr Gly Tyr Met Val Ala
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 Arg Ser Met Ala Leu Ala Pro Val Leu Ala Glu Ala Ile Val Glu Gly
 370 375 380
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 Leu Gly Ser Thr Arg Met Ile Arg Gly Ser Gln Leu Tyr His Arg Val
 385 390 395 400
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 Trp Asn Gly Leu Trp Pro Leu Asp Arg Arg Cys Val Arg Glu Cys Tyr
 405 410 415
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 Ser Phe Gly Met Glu Thr Leu Leu Lys Leu Asp Leu Lys Gly Thr Arg
 420 425 430
 Arg Leu Phe Asp Ala Phe Phe Asp Leu Asp Pro Lys Tyr Trp Gln Gly
 435 440 445
 25
 Phe Leu Ser Ser Arg Leu Ser Val Lys Glu Leu Gly Leu Leu Ser Leu
 450 455 460
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 Cys Leu Phe Gly His Gly Ser Asn Met Thr Arg Leu Asp Ile Val Thr
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25 acc tca cga act ttt tat ttc cgt cat tca ccg ttt ctt ggc cca aaa 100
 Thr Ser Arg Thr Phe Tyr Phe Arg His Ser Pro Phe Leu Gly Pro Lys
 15 20 25

30 cct act tcg aca acc tca cat gtt tct cca atc tct cct ttt tct ctt 148
 Pro Thr Ser Thr Thr Ser His Val Ser Pro Ile Ser Pro Phe Ser Leu
 30 35 40

35 aat cta ggc cca att ttg agg tct aga aga aaa ccc agt ttc act gtt 196
 Asn Leu Gly Pro Ile Leu Arg Ser Arg Arg Lys Pro Ser Phe Thr Val
 45 50 55

60 tgc ttt gtt ctc gag gat gag aag ctg aaa cct caa ttt gac gat gag 244
 Cys Phe Val Leu Glu Asp Glu Lys Leu Lys Pro Gln Phe Asp Asp Glu
 60 65 70 75

40 gct gag gat ttt gaa aag aag att gag gaa cag atc tta gct act cgc 292
 Ala Glu Asp Phe Glu Lys Lys Ile Glu Glu Gln Ile Leu Ala Thr Arg
 80 85 90

45 ttg gcg gag aaa ctg gct agg aag aaa tcg gag agg ttt act tat ctt 340
 Leu Ala Glu Lys Leu Ala Arg Lys Lys Ser Glu Arg Phe Thr Tyr Leu

	95	100	105	
	gtg gct gct ata atg tct agt ttt ggg att act tct atg gct gtt atg			388
	Val Ala Ala Ile Met Ser Ser Phe Gly Ile Thr Ser Met Ala Val Met			
5	110	115	120	
	gct gtt tat tac aga ttt tcg tgg caa atg gag gga gga gaa gtt cct			436
	Ala Val Tyr Tyr Arg Phe Ser Trp Gln Met Glu Gly Gly Glu Val Pro			
	125	130	135	
10				
	gta acc gaa atg ttg ggt aca ttt gct ctg tct gtt ggt gct gct gta			484
	Val Thr Glu Met Leu Gly Thr Phe Ala Leu Ser Val Gly Ala Ala Val			
	140	145	150	155
15				
	ggg atg gag ttt tgg gcg aga tgg gca cac aaa gca ctg tgg cat gct			532
	Gly Met Glu Phe Trp Ala Arg Trp Ala His Lys Ala Leu Trp His Ala			
		160	165	170
	tca cta tgg cac atg cat gag tca cac cac aaa cca aga gaa gga cct			580
20	Ser Leu Trp His Met His Glu Ser His His Lys Pro Arg Glu Gly Pro			
		175	180	185
	ttt gag ctg aac gac gtt ttc gcc ata aca aac gct gtt cca gca ata			628
	Phe Glu Leu Asn Asp Val Phe Ala Ile Thr Asn Ala Val Pro Ala Ile			
25	190	195	200	
	gcc ctg ctg aac tat ggt ttc ttc cat aaa ggc ctg att gcc gga cta			676
	Ala Leu Leu Asn Tyr Gly Phe Phe His Lys Gly Leu Ile Ala Gly Leu			
	205	210	215	
30				
	tgc ttc ggt gct ggg cta ggg atc aca gta ttt gga atg gca tac atg			724
	Cys Phe Gly Ala Gly Leu Gly Ile Thr Val Phe Gly Met Ala Tyr Met			
	220	225	230	235
35				
	ttt gtt cac gat ggt ttg gtt cac aag aga ttc cca gtt gga cct gta			772
	Phe Val His Asp Gly Leu Val His Lys Arg Phe Pro Val Gly Pro Val			
		240	245	250
	gcc aat gta cct tat ctt agg aag gtg gct gct gct cat tcg ctt cat			820
40	Ala Asn Val Pro Tyr Leu Arg Lys Val Ala Ala Ala His Ser Leu His			
		255	260	265
	cac tca gag aag ttc aat ggt gtc cca tat ggc ttg ttc ttc gga cct			868
	His Ser Glu Lys Phe Asn Gly Val Pro Tyr Gly Leu Phe Phe Gly Pro			
45	270	275	280	

aag gaa ctg gaa gaa gta gga ggg acg gaa gag ttg gaa aag gaa gtg 916
 Lys Glu Leu Glu Glu Val Gly Gly Thr Glu Glu Leu Glu Lys Glu Val
 285 290 295

5

ata cga agg acg aga ctt tcg aaa gga tca tgaacgattg ttcataaaca 966
 Ile Arg Arg Thr Arg Leu Ser Lys Gly Ser
 300 305

10

tagaattgtca ttttacactt cttatcaatg aggaaggggtg atttttgatg tatttgatag 1026
 tagagaaaaa tgtagctctc ttgatgaaat gaatttgat ttaatgtaggc tcttcttatt 1086
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<212> PRT

<213> Lycopersicon esculentum

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<400> 98

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Tyr Phe Arg His Ser Pro Phe Leu Gly Pro Lys Pro Thr Ser Thr Thr
 20 25 30

35

Ser His Val Ser Pro Ile Ser Pro Phe Ser Leu Asn Leu Gly Pro Ile
 35 40 45

40

Leu Arg Ser Arg Arg Lys Pro Ser Phe Thr Val Cys Phe Val Leu Glu
 50 55 60

45

Asp Glu Lys Leu Lys Pro Gln Phe Asp Asp Glu Ala Glu Asp Phe Glu

143

	65		70		75		80									
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				85					90					95		
10	Ala	Arg	Lys	Lys	Ser	Glu	Arg	Phe	Thr	Tyr	Leu	Val	Ala	Ala	Ile	Met
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15	Ser	Ser	Phe	Gly	Ile	Thr	Ser	Met	Ala	Val	Met	Ala	Val	Tyr	Tyr	Arg
			115					120					125			
20	Phe	Ser	Trp	Gln	Met	Glu	Gly	Gly	Glu	Val	Pro	Val	Thr	Glu	Met	Leu
			130				135						140			
25	Gly	Thr	Phe	Ala	Leu	Ser	Val	Gly	Ala	Ala	Val	Gly	Met	Glu	Phe	Trp
	145					150					155				160	
30	Ala	Arg	Trp	Ala	His	Lys	Ala	Leu	Trp	His	Ala	Ser	Leu	Trp	His	Met
				165					170					175		
35	His	Glu	Ser	His	His	Lys	Pro	Arg	Glu	Gly	Pro	Phe	Glu	Leu	Asn	Asp
			180						185					190		
40	Val	Phe	Ala	Ile	Thr	Asn	Ala	Val	Pro	Ala	Ile	Ala	Leu	Leu	Asn	Tyr
			195					200					205			
45	Gly	Phe	Phe	His	Lys	Gly	Leu	Ile	Ala	Gly	Leu	Cys	Phe	Gly	Ala	Gly
		210					215					220				
50	Leu	Gly	Ile	Thr	Val	Phe	Gly	Met	Ala	Tyr	Met	Phe	Val	His	Asp	Gly
	225					230				235				240		
55	Leu	Val	His	Lys	Arg	Phe	Pro	Val	Gly	Pro	Val	Ala	Asn	Val	Pro	Tyr
				245					250				255			

Leu Arg Lys Val Ala Ala Ala His Ser Leu His His Ser Glu Lys Phe
 260 265 270

5

Asn Gly Val Pro Tyr Gly Leu Phe Phe Gly Pro Lys Glu Leu Glu Glu
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Val Gly Gly Thr Glu Glu Leu Glu Lys Glu Val Ile Arg Arg Thr Arg
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15 Leu Ser Lys Gly Ser
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<210> 99

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<211> 1779

<212> DNA

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35 <223>

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aac tcc aac gga tct ttc cgt tct tat cag cct cgc act tcc gat gac 96
 45 Asn Ser Asn Gly Ser Phe Arg Ser Tyr Gln Pro Arg Thr Ser Asp Asp

	20	25	30	
5	gat cat cgt cgc cgg gct aca aca att gct cct cca ccg aaa gca tcc Asp His Arg Arg Arg Ala Thr Thr Ile Ala Pro Pro Pro Lys Ala Ser	144		
	35	40	45	
10	gac gcg ctt cct ctt ccg tta tat ctc aca aac gcc gtt ttc ttc acg Asp Ala Leu Pro Leu Pro Leu Tyr Leu Thr Asn Ala Val Phe Phe Thr	192		
	50	55	60	
15	ctc ttc ttc tcc gtc gcg tat tac ctc ctc cac cgg tgg cgt gac aag Leu Phe Phe Ser Val Ala Tyr Tyr Leu Leu His Arg Trp Arg Asp Lys	240		
	65	70	75	80
20	atc cgt tac aat acg cct ctt cac gtc gtc act atc aca gaa ctc ggc Ile Arg Tyr Asn Thr Pro Leu His Val Val Thr Ile Thr Glu Leu Gly	288		
	85	90	95	
25	gcc att att gct ctc atc gct tcg ttt atc tat ctc cta ggg ttt ttt Ala Ile Ile Ala Leu Ile Ala Ser Phe Ile Tyr Leu Leu Gly Phe Phe	336		
	100	105	110	
30	ggc att gac ttt gtt cag tca ttt atc tca cgt gcc tct ggt gat gct Gly Ile Asp Phe Val Gln Ser Phe Ile Ser Arg Ala Ser Gly Asp Ala	384		
	115	120	125	
35	tgg gat ctc gcc gat acg atc gat gat gat gac cac cgc ctt gtc acg Trp Asp Leu Ala Asp Thr Ile Asp Asp Asp Asp His Arg Leu Val Thr	432		
	130	135	140	
40	tgc tct cca ccg act ccg atc gtt tcc gtt gct aaa tta cct aat ccg Cys Ser Pro Pro Thr Pro Ile Val Ser Val Ala Lys Leu Pro Asn Pro	480		
	145	150	155	160
45	gaa cct att gtt acc gaa tcg ctt cct gag gaa gac gag gag att gtg Glu Pro Ile Val Thr Glu Ser Leu Pro Glu Glu Asp Glu Glu Ile Val	528		
	165	170	175	
50	aaa tcg gtt atc gac gga gtt att cca tcg tac tcg ctt gaa tct cgt Lys Ser Val Ile Asp Gly Val Ile Pro Ser Tyr Ser Leu Glu Ser Arg	576		
	180	185	190	
55	ctc ggt gat tgc aaa aga gcg gcg tcg att cgt cgt gag gcg ttg cag Leu Gly Asp Cys Lys Arg Ala Ala Ser Ile Arg Arg Glu Ala Leu Gln	624		
	195	200	205	

	aga gtc acc ggg aga tcg att gaa ggg tta ccg ttg gat gga ttt gat	672
	Arg Val Thr Gly Arg Ser Ile Glu Gly Leu Pro Leu Asp Gly Phe Asp	
	210 215 220	
5	tat gaa tcg att ttg ggg caa tgc tgt gag atg cct gtt gga tac att	720
	Tyr Glu Ser Ile Leu Gly Gln Cys Cys Glu Met Pro Val Gly Tyr Ile	
	225 230 235 240	
10	cag att cct gtt ggg att gct ggt cca ttg ttg ctt gat ggt tat gag	768
	Gln Ile Pro Val Gly Ile Ala Gly Pro Leu Leu Leu Asp Gly Tyr Glu	
	245 250 255	
15	tac tct gtt cct atg gct aca acc gaa ggt tgt ttg gtt gct agc act	816
	Tyr Ser Val Pro Met Ala Thr Thr Glu Gly Cys Leu Val Ala Ser Thr	
	260 265 270	
20	aac aga ggc tgc aag gct atg ttt atc tct ggt ggc gcc acc agt acc	864
	Asn Arg Gly Cys Lys Ala Met Phe Ile Ser Gly Gly Ala Thr Ser Thr	
	275 280 285	
25	gtt ctt aag gac ggt atg acc cga gca cct gtt gtt cgg ttc gct tcg	912
	Val Leu Lys Asp Gly Met Thr Arg Ala Pro Val Val Arg Phe Ala Ser	
	290 295 300	
30	gcg aga cga gct tcg gag ctt aag ttt ttc ttg gag aat cca gag aac	960
	Ala Arg Arg Ala Ser Glu Leu Lys Phe Phe Leu Glu Asn Pro Glu Asn	
	305 310 315 320	
35	ttt gat act ttg gca gta gtc ttc aac agg tcg agt aga ttt gca aga	1008
	Phe Asp Thr Leu Ala Val Val Phe Asn Arg Ser Ser Arg Phe Ala Arg	
	325 330 335	
40	ctg caa agt gtt aaa tgc aca atc gcg ggg aag aat gct tat gta agg	1056
	Leu Gln Ser Val Lys Cys Thr Ile Ala Gly Lys Asn Ala Tyr Val Arg	
	340 345 350	
45	ttc tgt tgt agt act ggt gat gct atg ggg atg aat atg gtt tct aaa	1104
	Phe Cys Cys Ser Thr Gly Asp Ala Met Gly Met Asn Met Val Ser Lys	
	355 360 365	
50	ggg gtg cag aat gtt ctt gag tat ctt acc gat gat ttc cct gac atg	1152
	Gly Val Gln Asn Val Leu Glu Tyr Leu Thr Asp Asp Phe Pro Asp Met	
	370 375 380	

147

	gat	gtg	att	gga	atc	tct	ggt	aac	ttc	tgt	tcg	gac	aag	aaa	cct	gct	1200
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	385					390				395					400		
5	gct	gtg	aac	tgg	att	gag	gga	cgt	ggt	aaa	tca	ggt	ggt	tgc	gag	gct	1248
	Ala	Val	Asn	Trp	Ile	Glu	Gly	Arg	Gly	Lys	Ser	Val	Val	Cys	Glu	Ala	
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10	Val	Ile	Arg	Gly	Glu	Ile	Val	Asn	Lys	Val	Leu	Lys	Thr	Ser	Val	Ala	
				420					425					430			
	gct	tta	gtc	gag	ctc	aac	atg	ctc	aag	aac	cta	gct	ggc	tct	gct	ggt	1344
15	Ala	Leu	Val	Glu	Leu	Asn	Met	Leu	Lys	Asn	Leu	Ala	Gly	Ser	Ala	Val	
		435						440					445				
	gca	ggc	tct	cta	ggt	gga	ttc	aac	gct	cat	gcc	agt	aac	ata	gtg	tct	1392
	Ala	Gly	Ser	Leu	Gly	Gly	Phe	Asn	Ala	His	Ala	Ser	Asn	Ile	Val	Ser	
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	Ala	Val	Phe	Ile	Ala	Thr	Gly	Gln	Asp	Pro	Ala	Gln	Asn	Val	Glu	Ser	
	465					470				475				480			
25	tct	caa	tgc	atc	acc	atg	atg	gaa	gct	att	aat	gac	ggc	aaa	gat	atc	1488
	Ser	Gln	Cys	Ile	Thr	Met	Met	Glu	Ala	Ile	Asn	Asp	Gly	Lys	Asp	Ile	
				485						490				495			
	cat	atc	tca	gtc	act	atg	cca	tct	atc	gag	gtg	ggg	aca	gtg	gga	gga	1536
30	His	Ile	Ser	Val	Thr	Met	Pro	Ser	Ile	Glu	Val	Gly	Thr	Val	Gly	Gly	
				500					505					510			
	gga	aca	cag	ctt	gca	tct	caa	tca	gcg	tgt	tta	aac	ctg	ctc	gga	ggt	1584
35	Gly	Thr	Gln	Leu	Ala	Ser	Gln	Ser	Ala	Cys	Leu	Asn	Leu	Leu	Gly	Val	
		515						520					525				
	aaa	gga	gca	agc	aca	gag	tcg	ccg	gga	atg	aac	gca	agg	agg	cta	gcg	1632
	Lys	Gly	Ala	Ser	Thr	Glu	Ser	Pro	Gly	Met	Asn	Ala	Arg	Arg	Leu	Ala	
		530					535					540					
40	acg	atc	gta	gcc	gga	gca	ggt	tta	gct	gga	gag	tta	tct	tta	atg	tca	1680
	Thr	Ile	Val	Ala	Gly	Ala	Val	Leu	Ala	Gly	Glu	Leu	Ser	Leu	Met	Ser	
	545					550				555				560			
45	gca	att	gca	gct	gga	cag	ctt	gtg	aga	agt	cac	atg	aaa	tac	aat	aga	1728

Ala Ile Ala Ala Gly Gln Leu Val Arg Ser His Met Lys Tyr Asn Arg
 565 570 575

tcc agc cga gac atc tct gga gca acg aca acg aca aca aca aca aca 1776
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tga 1779

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<212> PRT

<213> Arabidopsis thaliana

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<400> 100

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Asn Ser Asn Gly Ser Phe Arg Ser Tyr Gln Pro Arg Thr Ser Asp Asp
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Asp His Arg Arg Arg Ala Thr Thr Ile Ala Pro Pro Pro Lys Ala Ser
 35 40 45

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Asp Ala Leu Pro Leu Pro Leu Tyr Leu Thr Asn Ala Val Phe Phe Thr
 50 55 60

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Leu Phe Phe Ser Val Ala Tyr Tyr Leu Leu His Arg Trp Arg Asp Lys
 65 70 75 80

Ile Arg Tyr Asn Thr Pro Leu His Val Val Thr Ile Thr Glu Leu Gly
 85 90 95

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Ala Ile Ile Ala Leu Ile Ala Ser Phe Ile Tyr Leu Leu Gly Phe Phe
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5 Gly Ile Asp Phe Val Gln Ser Phe Ile Ser Arg Ala Ser Gly Asp Ala
115 120 125

10 Trp Asp Leu Ala Asp Thr Ile Asp Asp Asp Asp His Arg Leu Val Thr
130 135 140

Cys Ser Pro Pro Thr Pro Ile Val Ser Val Ala Lys Leu Pro Asn Pro
15 145 150 155 160

Glu Pro Ile Val Thr Glu Ser Leu Pro Glu Glu Asp Glu Glu Ile Val
165 170 175

20 Lys Ser Val Ile Asp Gly Val Ile Pro Ser Tyr Ser Leu Glu Ser Arg
180 185 190

25 Leu Gly Asp Cys Lys Arg Ala Ala Ser Ile Arg Arg Glu Ala Leu Gln
195 200 205

30 Arg Val Thr Gly Arg Ser Ile Glu Gly Leu Pro Leu Asp Gly Phe Asp
210 215 220

Tyr Glu Ser Ile Leu Gly Gln Cys Cys Glu Met Pro Val Gly Tyr Ile
35 225 230 235 240

Gln Ile Pro Val Gly Ile Ala Gly Pro Leu Leu Leu Asp Gly Tyr Glu
245 250 255

40 Tyr Ser Val Pro Met Ala Thr Thr Glu Gly Cys Leu Val Ala Ser Thr
260 265 270

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150

	Asn	Arg	Gly	Cys	Lys	Ala	Met	Phe	Ile	Ser	Gly	Gly	Ala	Thr	Ser	Thr
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5	Val	Leu	Lys	Asp	Gly	Met	Thr	Arg	Ala	Pro	Val	Val	Arg	Phe	Ala	Ser
	290						295					300				
10	Ala	Arg	Arg	Ala	Ser	Glu	Leu	Lys	Phe	Phe	Leu	Glu	Asn	Pro	Glu	Asn
	305					310					315				320	
15	Phe	Asp	Thr	Leu	Ala	Val	Val	Phe	Asn	Arg	Ser	Ser	Arg	Phe	Ala	Arg
				325					330					335		
20	Leu	Gln	Ser	Val	Lys	Cys	Thr	Ile	Ala	Gly	Lys	Asn	Ala	Tyr	Val	Arg
		340						345					350			
25	Phe	Cys	Cys	Ser	Thr	Gly	Asp	Ala	Met	Gly	Met	Asn	Met	Val	Ser	Lys
		355						360				365				
30	Gly	Val	Gln	Asn	Val	Leu	Glu	Tyr	Leu	Thr	Asp	Asp	Phe	Pro	Asp	Met
		370				375						380				
35	Asp	Val	Ile	Gly	Ile	Ser	Gly	Asn	Phe	Cys	Ser	Asp	Lys	Lys	Pro	Ala
	385					390				395					400	
40	Ala	Val	Asn	Trp	Ile	Glu	Gly	Arg	Gly	Lys	Ser	Val	Val	Cys	Glu	Ala
			405					410						415		
45	Val	Ile	Arg	Gly	Glu	Ile	Val	Asn	Lys	Val	Leu	Lys	Thr	Ser	Val	Ala
		420						425					430			
50	Ala	Leu	Val	Glu	Leu	Asn	Met	Leu	Lys	Asn	Leu	Ala	Gly	Ser	Ala	Val
		435					440					445				
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151

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455

460

Ala Val Phe Ile Ala Thr Gly Gln Asp Pro Ala Gln Asn Val Glu Ser
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Ser Gln Cys Ile Thr Met Met Glu Ala Ile Asn Asp Gly Lys Asp Ile
10 485 490 495

His Ile Ser Val Thr Met Pro Ser Ile Glu Val Gly Thr Val Gly Gly
500 505 510

15 Gly Thr Gln Leu Ala Ser Gln Ser Ala Cys Leu Asn Leu Leu Gly Val
515 520 525

20 Lys Gly Ala Ser Thr Glu Ser Pro Gly Met Asn Ala Arg Arg Leu Ala
530 535 540

25 Thr Ile Val Ala Gly Ala Val Leu Ala Gly Glu Leu Ser Leu Met Ser
545 550 555 560

Ala Ile Ala Ala Gly Gln Leu Val Arg Ser His Met Lys Tyr Asn Arg
565 570 575
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Ser Ser Arg Asp Ile Ser Gly Ala Thr Thr Thr Thr Thr Thr Thr Thr
580 585 590

35 <210> 101

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ttc gtg cgg gag aat cat ctc tct gga tcc gga tct ctc cgc cgc cgg 96
 Phe Val Arg Glu Asn His Leu Ser Gly Ser Gly Ser Leu Arg Arg Arg
 20 25 30

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aaa gct tta tca gtc cgg tgc tcg tct ggc gat gag aac gct cct tcg 144
 Lys Ala Leu Ser Val Arg Cys Ser Ser Gly Asp Glu Asn Ala Pro Ser
 35 40 45

25

cca tcg gtg gtg atg gac tcc gat ttc gac gcc aag gtg ttc cgt aag 192
 Pro Ser Val Val Met Asp Ser Asp Phe Asp Ala Lys Val Phe Arg Lys
 50 55 60

30

aac ttg acg aga agc gat aat tac aat cgt aaa ggg ttc ggt cat aag 240
 Asn Leu Thr Arg Ser Asp Asn Tyr Asn Arg Lys Gly Phe Gly His Lys
 65 70 75 80

35

gag gag aca ctc aag ctc atg aat cga gag tac acc agt gat ata ttg 288
 Glu Glu Thr Leu Lys Leu Met Asn Arg Glu Tyr Thr Ser Asp Ile Leu
 85 90 95

40

gag aca ctg aaa aca aat ggg tat act tat tct tgg gga gat gtt act 336
 Glu Thr Leu Lys Thr Asn Gly Tyr Thr Tyr Ser Trp Gly Asp Val Thr
 100 105 110

45

gtg aaa ctc gct aaa gca tat ggt ttt tgc tgg ggt gtt gag cgt gct 384
 Val Lys Leu Ala Lys Ala Tyr Gly Phe Cys Trp Gly Val Glu Arg Ala
 115 120 125

gtt cag att gca tat gaa gca cga aag cag ttt cca gag gag agg ctt 432
 Val Gln Ile Ala Tyr Glu Ala Arg Lys Gln Phe Pro Glu Glu Arg Leu

153

	130	135	140	
	tgg att act aac gaa atc att cat aac ccg acc gtc aat aag agg ttg			480
	Trp Ile Thr Asn Glu Ile Ile His Asn Pro Thr Val Asn Lys Arg Leu			
5	145	150	155	160
	gaa gat atg gat gtt aaa att att ccg gtt gag gat tca aag aaa cag			528
	Glu Asp Met Asp Val Lys Ile Ile Pro Val Glu Asp Ser Lys Lys Gln			
		165	170	175
10				
	ttt gat gta gta gag aaa gat gat gtg gtt atc ctt cct gcg ttt gga			576
	Phe Asp Val Val Glu Lys Asp Asp Val Val Ile Leu Pro Ala Phe Gly			
		180	185	190
	gct ggt gtt gac gag atg tat gtt ctt aat gat aaa aag gtg caa att			624
15	Ala Gly Val Asp Glu Met Tyr Val Leu Asn Asp Lys Lys Val Gln Ile			
		195	200	205
	gtt gac acg act tgt cct tgg gtg aca aag gtc tgg aac acg gtt gag			672
20	Val Asp Thr Thr Cys Pro Trp Val Thr Lys Val Trp Asn Thr Val Glu			
		210	215	220
	aag cac aag aag ggg gaa tac aca tca gta atc cat ggt aaa tat aat			720
	Lys His Lys Lys Gly Glu Tyr Thr Ser Val Ile His Gly Lys Tyr Asn			
25	225	230	235	240
	cat gaa gag acg att gca act gcg tct ttt gca gga aag tac atc att			768
	His Glu Glu Thr Ile Ala Thr Ala Ser Phe Ala Gly Lys Tyr Ile Ile			
		245	250	255
30				
	gta aag aac atg aaa gag gca aat tac gtt tgt gat tac att ctc ggt			816
	Val Lys Asn Met Lys Glu Ala Asn Tyr Val Cys Asp Tyr Ile Leu Gly			
		260	265	270
	ggc caa tac gat gga tct agc tcc aca aaa gag gag ttc atg gag aaa			864
35	Gly Gln Tyr Asp Gly Ser Ser Ser Thr Lys Glu Glu Phe Met Glu Lys			
		275	280	285
	ttc aaa tac gca att tcg aag ggt ttc gat ccc gac aat gac ctt gtc			912
40	Phe Lys Tyr Ala Ile Ser Lys Gly Phe Asp Pro Asp Asn Asp Leu Val			
		290	295	300
	aaa gtt ggt att gca aac caa aca acg atg cta aag gga gaa aca gag			960
	Lys Val Gly Ile Ala Asn Gln Thr Thr Met Leu Lys Gly Glu Thr Glu			
45	305	310	315	320

	gag ata gga aga tta ctc gag aca aca atg atg cgc aag tat gga gtg	1008
	Glu Ile Gly Arg Leu Leu Glu Thr Thr Met Met Arg Lys Tyr Gly Val	
	325 330 335	
5	gaa aat gta agc gga cat ttc atc agc ttc aac aca ata tgc gac gtt	1056
	Glu Asn Val Ser Gly His Phe Ile Ser Phe Asn Thr Ile Cys Asp Ala	
	340 345 350	
10	act caa gag cga caa gac gca atc tat gag cta gtg gaa gag aag att	1104
	Thr Gln Glu Arg Gln Asp Ala Ile Tyr Glu Leu Val Glu Glu Lys Ile	
	355 360 365	
	gac ctc atg gta gtg gtt ggc gga tgg aat tca agt aac acc tct cac	1152
15	Asp Leu Met Leu Val Val Gly Gly Trp Asn Ser Ser Asn Thr Ser His	
	370 375 380	
	ctt cag gaa atc tca gag gca cgg gga atc cca tct tac tgg atc gat	1200
	Leu Gln Glu Ile Ser Glu Ala Arg Gly Ile Pro Ser Tyr Trp Ile Asp	
20	385 390 395 400	
	agt gag aaa cgg ata gga cct ggg aat aaa ata gcc tat aag ctc cac	1248
	Ser Glu Lys Arg Ile Gly Pro Gly Asn Lys Ile Ala Tyr Lys Leu His	
	405 410 415	
25	tat gga gaa ctg gtc gag aag gaa aac ttt ctc cca aag gga cca ata	1296
	Tyr Gly Glu Leu Val Glu Lys Glu Asn Phe Leu Pro Lys Gly Pro Ile	
	420 425 430	
30	aca atc ggt gtg aca tca ggt gca tca acc ccg gat aag gtc gtg gaa	1344
	Thr Ile Gly Val Thr Ser Gly Ala Ser Thr Pro Asp Lys Val Val Glu	
	435 440 445	
	gat gct ttg gtg aag gtg ttc gac att aaa cgt gaa gag tta ttg cag	1392
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<211> 466

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5 <213> Arabidopsis thaliana ISPH

<400> 102

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Met Ala Val Ala Leu Gln Phe Ser Arg Leu Cys Val Arg Pro Asp Thr
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Phe Val Arg Glu Asn His Leu Ser Gly Ser Gly Ser Leu Arg Arg Arg
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20

Lys Ala Leu Ser Val Arg Cys Ser Ser Gly Asp Glu Asn Ala Pro Ser
 35 40 45

25

Pro Ser Val Val Met Asp Ser Asp Phe Asp Ala Lys Val Phe Arg Lys
 50 55 60

30

Asn Leu Thr Arg Ser Asp Asn Tyr Asn Arg Lys Gly Phe Gly His Lys
 65 70 75 80

35

Glu Glu Thr Leu Lys Leu Met Asn Arg Glu Tyr Thr Ser Asp Ile Leu
 85 90 95

40

Glu Thr Leu Lys Thr Asn Gly Tyr Thr Tyr Ser Trp Gly Asp Val Thr
 100 105 110

Val Lys Leu Ala Lys Ala Tyr Gly Phe Cys Trp Gly Val Glu Arg Ala
 115 120 125

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Val Gln Ile Ala Tyr Glu Ala Arg Lys Gln Phe Pro Glu Glu Arg Leu
 130 135 140

Trp Ile Thr Asn Glu Ile Ile His Asn Pro Thr Val Asn Lys Arg Leu
 145 150 155 160

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Glu Asp Met Asp Val Lys Ile Ile Pro Val Glu Asp Ser Lys Lys Gln
 165 170 175

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Phe Asp Val Val Glu Lys Asp Asp Val Val Ile Leu Pro Ala Phe Gly
 180 185 190

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Ala Gly Val Asp Glu Met Tyr Val Leu Asn Asp Lys Lys Val Gln Ile
 195 200 205

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Val Asp Thr Thr Cys Pro Trp Val Thr Lys Val Trp Asn Thr Val Glu
 210 215 220

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Lys His Lys Lys Gly Glu Tyr Thr Ser Val Ile His Gly Lys Tyr Asn
 225 230 235 240

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His Glu Glu Thr Ile Ala Thr Ala Ser Phe Ala Gly Lys Tyr Ile Ile
 245 250 255

35

Val Lys Asn Met Lys Glu Ala Asn Tyr Val Cys Asp Tyr Ile Leu Gly
 260 265 270

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Gly Gln Tyr Asp Gly Ser Ser Ser Thr Lys Glu Glu Phe Met Glu Lys
 275 280 285

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Phe Lys Tyr Ala Ile Ser Lys Gly Phe Asp Pro Asp Asn Asp Leu Val
 290 295 300

Lys Val Gly Ile Ala Asn Gln Thr Thr Met Leu Lys Gly Glu Thr Glu
 305 310 315 320

157

Glu Ile Gly Arg Leu Leu Glu Thr Thr Met Met Arg Lys Tyr Gly Val
 325 330 335

5 Glu Asn Val Ser Gly His Phe Ile Ser Phe Asn Thr Ile Cys Asp Ala
 340 345 350

10 Thr Gln Glu Arg Gln Asp Ala Ile Tyr Glu Leu Val Glu Glu Lys Ile
 355 360 365

15 Asp Leu Met Leu Val Val Gly Gly Trp Asn Ser Ser Asn Thr Ser His
 370 375 380

Leu Gln Glu Ile Ser Glu Ala Arg Gly Ile Pro Ser Tyr Trp Ile Asp
 385 390 395 400

20 Ser Glu Lys Arg Ile Gly Pro Gly Asn Lys Ile Ala Tyr Lys Leu His
 405 410 415

25 Tyr Gly Glu Leu Val Glu Lys Glu Asn Phe Leu Pro Lys Gly Pro Ile
 420 425 430

30 Thr Ile Gly Val Thr Ser Gly Ala Ser Thr Pro Asp Lys Val Val Glu
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Leu Ala
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40 <210> 103
 <211> 2160

<212> DNA

<213> Lycopersicon esculentum

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gtg gtt tca gat tct tct aag gca acc cct ttg ttc tct gga tgg att 96
 Val Val Ser Asp Ser Ser Lys Ala Thr Pro Leu Phe Ser Gly Trp Ile
 20 25 30

cat gga aca gat ctg cag ttt ttg ttc caa cac aag ctt act cat gag 144
 His Gly Thr Asp Leu Gln Phe Leu Phe Gln His Lys Leu Thr His Glu
 35 40 45

gtc aag aaa agg tca cgt gtg gtt cag gct tcc tta tca gaa tct gga 192
 Val Lys Lys Arg Ser Arg Val Val Gln Ala Ser Leu Ser Glu Ser Gly
 50 55 60

gaa tac tac aca cag aga ccg cca acg cct att ttg gac act gtg aac 240
 Glu Tyr Tyr Thr Gln Arg Pro Pro Thr Pro Ile Leu Asp Thr Val Asn
 65 70 75 80

tat ccc att cat atg aaa aat ctg tct ctg aag gaa ctt aaa caa cta 288
 Tyr Pro Ile His Met Lys Asn Leu Ser Leu Lys Glu Leu Lys Gln Leu
 40 85 90 95

gca gat gaa cta agg tca gat aca att ttc aat gta tca aag act ggg 336
 Ala Asp Glu Leu Arg Ser Asp Thr Ile Phe Asn Val Ser Lys Thr Gly
 100 105 110

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	ggt cac ctt ggc tca agt ctt ggt gtt gtt gag ctg act gtt gct ctt Gly His Leu Gly Ser Ser Leu Gly Val Val Glu Leu Thr Val Ala Leu 115 120 125	384
5	cat tat gtc ttc aat gca ccg caa gat agg att ctc tgg gat gtt ggt His Tyr Val Phe Asn Ala Pro Gln Asp Arg Ile Leu Trp Asp Val Gly 130 135 140	432
10	cat cag tct tat cct cac aaa atc ttg act ggt aga agg gac aag atg His Gln Ser Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Asp Lys Met 145 150 155 160	480
15	tcg aca tta agg cag aca gat ggt ctt gca gga ttt act aag cga tcg Ser Thr Leu Arg Gln Thr Asp Gly Leu Ala Gly Phe Thr Lys Arg Ser 165 170 175	528
20	gag agt gaa tat gat tgc ttt ggc acc ggc cac agt tcc acc acc atc Glu Ser Glu Tyr Asp Cys Phe Gly Thr Gly His Ser Ser Thr Thr Ile 180 185 190	576
	tca gca ggc cta ggg atg gct gtt ggt aga gat cta aaa gga aga aac Ser Ala Gly Leu Gly Met Ala Val Gly Arg Asp Leu Lys Gly Arg Asn 195 200 205	624
25	aac aat gtt att gcc gta ata ggt gat ggt gcc atg aca gca ggt caa Asn Asn Val Ile Ala Val Ile Gly Asp Gly Ala Met Thr Ala Gly Gln 210 215 220	672
30	gct tat gaa gcc atg aat aat gct ggt tac ctg gac tct gac atg att Ala Tyr Glu Ala Met Asn Asn Ala Gly Tyr Leu Asp Ser Asp Met Ile 225 230 235 240	720
35	ggt atc tta aac gac aat aga caa gtt tct tta cct act gct act ctg Val Ile Leu Asn Asp Asn Arg Gln Val Ser Leu Pro Thr Ala Thr Leu 245 250 255	768
40	gat ggg cca gtt gct cct gtt gga gct cta agt agt gct ttg agc agg Asp Gly Pro Val Ala Pro Val Gly Ala Leu Ser Ser Ala Leu Ser Arg 260 265 270	816
	tta cag tct aat agg cct ctc aga gaa cta aga gaa gtc gca aag gga Leu Gln Ser Asn Arg Pro Leu Arg Glu Leu Arg Glu Val Ala Lys Gly 275 280 285	864
45	ggt act aag cag att ggt ggt cct atg cat gag ctt gct gca aaa gtt	912

160

	Val Thr Lys Gln Ile Gly Gly Pro Met His Glu Leu Ala Ala Lys Val	
	290 295 300	
5	gat gaa tat gct cgt ggc atg att agt ggt tct gga tca aca ttg ttt Asp Glu Tyr Ala Arg Gly Met Ile Ser Gly Ser Gly Ser Thr Leu Phe	960
	305 310 315 320	
10	gaa gaa ctt gga ctt tac tat att ggt cct gtg gat ggt cac aac att Glu Glu Leu Gly Leu Tyr Tyr Ile Gly Pro Val Asp Gly His Asn Ile	1008
	325 330 335	
15	gat gat cta att gcg att ctc aaa gag gtt aga agt act aaa aca aca Asp Asp Leu Ile Ala Ile Leu Lys Glu Val Arg Ser Thr Lys Thr Thr	1056
	340 345 350	
20	ggg cca gta ctg atc cat gtt gtc act gag aaa ggc aga ggt tat cca Gly Pro Val Leu Ile His Val Val Thr Glu Lys Gly Arg Gly Tyr Pro	1104
	355 360 365	
25	tat gct gag aga gct gca gat aag tat cat gga gtt gcc aag ttt gat Tyr Ala Glu Arg Ala Ala Asp Lys Tyr His Gly Val Ala Lys Phe Asp	1152
	370 375 380	
30	cca gca aca gga aag caa ttc aaa gcc agt gcc aag aca cag tcc tat Pro Ala Thr Gly Lys Gln Phe Lys Ala Ser Ala Lys Thr Gln Ser Tyr	1200
	385 390 395 400	
35	aca aca tat ttt gcc gag gct tta att gca gaa gca gaa gca gat aaa Thr Thr Tyr Phe Ala Glu Ala Leu Ile Ala Glu Ala Glu Ala Asp Lys	1248
	405 410 415	
40	gac att gtt gca atc cat gct gcc atg ggg ggt ggg acc gga atg aac Asp Ile Val Ala Ile His Ala Ala Met Gly Gly Gly Thr Gly Met Asn	1296
	420 425 430	
45	ctt ttc cat cgt cgc ttc cca aca agg tgt ttt gat gtt gga ata gca Leu Phe His Arg Arg Phe Pro Thr Arg Cys Phe Asp Val Gly Ile Ala	1344
	435 440 445	
50	gaa caa cat gca gta acc ttt gct gct gga ttg gct tgt gaa ggc att Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Cys Glu Gly Ile	1392
	450 455 460	
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161

	465	470	475	480	
	cag gta gtg cat gac gtt gat ttg caa aag ctg ccc gtg agg ttt gca	1488			
	Gln Val Val His Asp Val Asp Leu Gln Lys Leu Pro Val Arg Phe Ala				
5	485	490	495		
	atg gac aga gca ggt ctt gtt gga gca gat ggt cca aca cat tgt ggt	1536			
	Met Asp Arg Ala Gly Leu Val Gly Ala Asp Gly Pro Thr His Cys Gly				
	500	505	510		
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	gca ttt gat gtt act tac atg gca tgt ctt cct aac atg gtt gta atg	1584			
	Ala Phe Asp Val Thr Tyr Met Ala Cys Leu Pro Asn Met Val Val Met				
	515	520	525		
15					
	gct cct tct gat gaa gcg gag cta ttt cac atg gta gca act gct gcc	1632			
	Ala Pro Ser Asp Glu Ala Glu Leu Phe His Met Val Ala Thr Ala Ala				
	530	535	540		
20					
	gcc att gat gac aga cca agt tgt ttt aga tac cca aga gga aat ggg	1680			
	Ala Ile Asp Asp Arg Pro Ser Cys Phe Arg Tyr Pro Arg Gly Asn Gly				
	545	550	555	560	
	atc ggt gta gag ctt ccg gct gga aac aaa gga att cct ctt gag gtt	1728			
	Ile Gly Val Glu Leu Pro Ala Gly Asn Lys Gly Ile Pro Leu Glu Val				
25	565	570	575		
	ggt aaa ggt agg ata ttg att gag ggg gag aga gtg gct cta ttg gga	1776			
	Gly Lys Gly Arg Ile Leu Ile Glu Gly Glu Arg Val Ala Leu Leu Gly				
	580	585	590		
30					
	tat ggc tca gca gtg cag aac tgt ttg gat gct gct att gtg cta gaa	1824			
	Tyr Gly Ser Ala Val Gln Asn Cys Leu Asp Ala Ala Ile Val Leu Glu				
	595	600	605		
35					
	tcc cgc ggc tta caa gta aca gtt gca gat gca cgt ttc tgc aaa cca	1872			
	Ser Arg Gly Leu Gln Val Thr Val Ala Asp Ala Arg Phe Cys Lys Pro				
	610	615	620		
40					
	ctg gac cat gcc ctc ata agg agc ctt gca aaa tca cat gaa gtg cta	1920			
	Leu Asp His Ala Leu Ile Arg Ser Leu Ala Lys Ser His Glu Val Leu				
	625	630	635	640	
	atc act gtc gaa gaa gga tca att gga ggt ttt gga tct cat gtt gtt	1968			
	Ile Thr Val Glu Glu Gly Ser Ile Gly Gly Phe Gly Ser His Val Val				
45	645	650	655		

5 cag ttc atg gcc tta gat ggg ctt ctt gat ggc aag ttg aag tgg aga 2016
 Gln Phe Met Ala Leu Asp Gly Leu Leu Asp Gly Lys Leu Lys Trp Arg
 660 665 670

10 cca ata gtt ctt cct gat cga tac att gac cat gga tct cct gtt gat 2064
 Pro Ile Val Leu Pro Asp Arg Tyr Ile Asp His Gly Ser Pro Val Asp
 675 680 685

15 cag ttg gcg gaa gct ggc cta aca cca tct cac att gca gca aca gta 2112
 Gln Leu Ala Glu Ala Gly Leu Thr Pro Ser His Ile Ala Ala Thr Val
 690 695 700

20 ttt aac ata ctt gga caa acc aga gag gct cta gag gtc atg aca taa 2160
 Phe Asn Ile Leu Gly Gln Thr Arg Glu Ala Leu Glu Val Met Thr
 705 710 715

<210> 104

<211> 719

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25 <213> Lycopersicon esculentum

30 <400> 104

Met Ala Leu Cys Ala Tyr Ala Phe Pro Gly Ile Leu Asn Arg Thr Gly
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 20 25 30

40 His Gly Thr Asp Leu Gln Phe Leu Phe Gln His Lys Leu Thr His Glu
 35 40 45

45 Val Lys Lys Arg Ser Arg Val Val Gln Ala Ser Leu Ser Glu Ser Gly
 50 55 60

Glu Tyr Tyr Thr Gln Arg Pro Pro Thr Pro Ile Leu Asp Thr Val Asn
 65 70 75 80

5

Tyr Pro Ile His Met Lys Asn Leu Ser Leu Lys Glu Leu Lys Gln Leu
 85 90 95

10

Ala Asp Glu Leu Arg Ser Asp Thr Ile Phe Asn Val Ser Lys Thr Gly
 100 105 110

15

Gly His Leu Gly Ser Ser Leu Gly Val Val Glu Leu Thr Val Ala Leu
 115 120 125

20

His Tyr Val Phe Asn Ala Pro Gln Asp Arg Ile Leu Trp Asp Val Gly
 130 135 140

His Gln Ser Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Asp Lys Met
 145 150 155 160

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Ser Thr Leu Arg Gln Thr Asp Gly Leu Ala Gly Phe Thr Lys Arg Ser
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Glu Ser Glu Tyr Asp Cys Phe Gly Thr Gly His Ser Ser Thr Thr Ile
 180 185 190

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Ser Ala Gly Leu Gly Met Ala Val Gly Arg Asp Leu Lys Gly Arg Asn
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Asn Asn Val Ile Ala Val Ile Gly Asp Gly Ala Met Thr Ala Gly Gln
 210 215 220

Ala Tyr Glu Ala Met Asn Asn Ala Gly Tyr Leu Asp Ser Asp Met Ile
 225 230 235 240

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164

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5	Asp	Gly	Pro	Val	Ala	Pro	Val	Gly	Ala	Leu	Ser	Ser	Ala	Leu	Ser	Arg	
					260				265					270			
10	Leu	Gln	Ser	Asn	Arg	Pro	Leu	Arg	Glu	Leu	Arg	Glu	Val	Ala	Lys	Gly	
				275				280					285				
15	Val	Thr	Lys	Gln	Ile	Gly	Gly	Pro	Met	His	Glu	Leu	Ala	Ala	Lys	Val	
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25	Glu	Glu	Leu	Gly	Leu	Tyr	Tyr	Ile	Gly	Pro	Val	Asp	Gly	His	Asn	Ile	
					325					330				335			
30	Asp	Asp	Leu	Ile	Ala	Ile	Leu	Lys	Glu	Val	Arg	Ser	Thr	Lys	Thr	Thr	
				340					345					350			
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		355					360						365				
40	Tyr	Ala	Glu	Arg	Ala	Ala	Asp	Lys	Tyr	His	Gly	Val	Ala	Lys	Phe	Asp	
	370						375					380					
45	Pro	Ala	Thr	Gly	Lys	Gln	Phe	Lys	Ala	Ser	Ala	Lys	Thr	Gln	Ser	Tyr	
	385				390					395					400		
50	Thr	Thr	Tyr	Phe	Ala	Glu	Ala	Leu	Ile	Ala	Glu	Ala	Glu	Ala	Asp	Lys	
				405					410					415			
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420

425

430

5 Leu Phe His Arg Arg Phe Pro Thr Arg Cys Phe Asp Val Gly Ile Ala
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10 Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Cys Glu Gly Ile
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465 470 475 480

Gln Val Val His Asp Val Asp Leu Gln Lys Leu Pro Val Arg Phe Ala
485 490 495

20 Met Asp Arg Ala Gly Leu Val Gly Ala Asp Gly Pro Thr His Cys Gly
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25 Ala Phe Asp Val Thr Tyr Met Ala Cys Leu Pro Asn Met Val Val Met
515 520 525

30 Ala Pro Ser Asp Glu Ala Glu Leu Phe His Met Val Ala Thr Ala Ala
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35 Ala Ile Asp Asp Arg Pro Ser Cys Phe Arg Tyr Pro Arg Gly Asn Gly
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Ile Gly Val Glu Leu Pro Ala Gly Asn Lys Gly Ile Pro Leu Glu Val
565 570 575

40 Gly Lys Gly Arg Ile Leu Ile Glu Gly Glu Arg Val Ala Leu Leu Gly
580 585 590

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595 600 605

Ser Arg Gly Leu Gln Val Thr Val Ala Asp Ala Arg Phe Cys Lys Pro
 610 615 620
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Leu Asp His Ala Leu Ile Arg Ser Leu Ala Lys Ser His Glu Val Leu
 625 630 635 640

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Ile Thr Val Glu Glu Gly Ser Ile Gly Gly Phe Gly Ser His Val Val
 645 650 655

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Gln Phe Met Ala Leu Asp Gly Leu Leu Asp Gly Lys Leu Lys Trp Arg
 660 665 670

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Pro Ile Val Leu Pro Asp Arg Tyr Ile Asp His Gly Ser Pro Val Asp
 675 680 685

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Gln Leu Ala Glu Ala Gly Leu Thr Pro Ser His Ile Ala Ala Thr Val
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Phe Leu Asp Thr Ser Arg Phe Asn Pro Ile Pro Lys Leu Ser Gly Gly
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Phe Ser Leu Arg Arg Arg Asn Gln Gly Arg Gly Phe Gly Lys Gly Val
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20 aag tgt tca gtg aaa gtg cag cag caa caa cca cct cct cca gca tgg 192
 Lys Cys Ser Val Lys Val Gln Gln Gln Gln Gln Pro Pro Pro Ala Trp
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25 cct ggg aga gct gtc cct gag gcg cct cgt caa tct tgg gat gga cca 240
Pro Gly Arg Ala Val Pro Glu Ala Pro Arg Gln Ser Trp Asp Gly Pro
65 70 75 80

aaa ccc atc tct atc gtt gga tct act ggt tct att ggc act cag aca 288
Lys Pro Ile Ser Ile Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr
30 85 90 95

ttg gat att gtg gct gag aat cct gac aaa ttc aga gtt gtg gct cta 336
Leu Asp, Ile Val Ala Glu Asn Pro Asp Lys Phe Arg Val Val Ala Leu
100 105 110

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gct gct ggt tgc aat gtt act cta ctt gct gat cag gta agg aga ttt 384
Ala Ala Gly Ser Asn Val Thr Leu Leu Ala Asp Gln Val Arg Arg Phe
115 120 125

40 aag cct gca ttg gtt gct gtt aga aac gag tca ctg att aat gag ctt 432
 Lys Pro Ala Leu Val Ala Val Arg Asn Glu Ser Leu Ile Asn Glu Leu
 130 135 140

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Lys Glu Ala Leu Ala Asp Leu Asp Tyr Lys Leu Glu Ile Ile Pro Gly

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	Glu Gln Gly Val Ile Glu Val Ala Arg His Pro Glu Ala Val Thr Val				
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	gtt acc gga ata gta ggt tgt gcg gga cta aag cct acg gtt gct gca				576
	Val Thr Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala				
		180	185	190	
10	att gaa gca gga aag gac att gct ctt gca aac aaa gag aca tta atc				624
	Ile Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile				
		195	200	205	
15	gca ggt ggt cct ttc gtg ctt ccg ctt gcc aac aaa cat aat gta aag				672
	Ala Gly Gly Pro Phe Val Leu Pro Leu Ala Asn Lys His Asn Val Lys				
		210	215	220	
	att ctt ccg gca gat tca gaa cat tct gcc ata ttt cag tgt att caa				720
20	Ile Leu Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln				
		225	230	235	240
	ggt ttg cct gaa ggc gct ctg cgc aag ata atc ttg act gca tct ggt				768
	Gly Leu Pro Glu Gly Ala Leu Arg Lys Ile Ile Leu Thr Ala Ser Gly				
25		245	250	255	
	gga gct ttt agg gat tgg cct gtc gaa aag cta aag gaa gtt aaa gta				816
	Gly Ala Phe Arg Asp Trp Pro Val Glu Lys Leu Lys Glu Val Lys Val				
		260	265	270	
30	gcg gat gcg ttg aag cat cca aac tgg aac atg gga aag aaa atc act				864
	Ala Asp Ala Leu Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr				
		275	280	285	
35	gtg gac tct gct acg ctt ttc aac aag ggt ctt gag gtc att gaa gcg				912
	Val Asp Ser Ala Thr Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala				
		290	295	300	
	cat tat ttg ttt gga gct gag tat gac gat ata gag att gtc att cat				960
40	His Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His				
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	ccg caa agt atc ata cat tcc atg att gaa aca cag gat tca tct gtg				1008
	Pro Gln Ser Ile Ile His Ser Met Ile Glu Thr Gln Asp Ser Ser Val				
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	ctt gct caa ttg ggt tgg cct gat atg cgt tta ccg att ctc tac acc	1056
	Leu Ala Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr	
	340 345 350	
5	atg tca tgg ccc gat aga gtt cct tgt tct gaa gta act tgg cca aga	1104
	Met Ser Trp Pro Asp Arg Val Pro Cys Ser Glu Val Thr Trp Pro Arg	
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10	ctt gac ctt tgc aaa ctc ggt tca ttg act ttc aag aaa cca gac aat	1152
	Leu Asp Leu Cys Lys Leu Gly Ser Leu Thr Phe Lys Lys Pro Asp Asn	
	370 375 380	
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15	Val Lys Tyr Pro Ser Met Asp Leu Ala Tyr Ala Ala Gly Arg Ala Gly	
	385 390 395 400	
	ggc aca atg act gga gtt ctc agc gcc gcc aat gag aaa gct gtt gaa	1248
	Gly Thr Met Thr Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu	
20	405 410 415	
	atg ttc att gat gaa aag ata agc tat ttg gat atc ttc aag gtt gtg	1296
	Met Phe Ile Asp Glu Lys Ile Ser Tyr Leu Asp Ile Phe Lys Val Val	
	420 425 430	
25	gaa tta aca tgc gat aaa cat cga aac gag ttg gta aca tca ccg tct	1344
	Glu Leu Thr Cys Asp Lys His Arg Asn Glu Leu Val Thr Ser Pro Ser	
	435 440 445	
30	ctt gaa gag att gtt cac tat gac ttg tgg gca cgt gaa tat gcc gcg	1392
	Leu Glu Glu Ile Val His Tyr Asp Leu Trp Ala Arg Glu Tyr Ala Ala	
	450 455 460	
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Phe Ser Leu Arg Arg Arg Asn Gln Gly Arg Gly Phe Gly Lys Gly Val

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Lys Cys Ser Val Lys Val Gln Gln Gln Gln Gln Pro Pro Ala Trp

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Pro Gly Arg Ala Val Pro Glu Ala Pro Arg Gln Ser Trp Asp Gly Pro

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Lys Pro Ile Ser Ile Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr

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90

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Leu Asp Ile Val Ala Glu Asn Pro Asp Lys Phe Arg Val Val Ala Leu

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Ala Ala Gly Ser Asn Val Thr Leu Leu Ala Asp Gln Val Arg Arg Phe

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Lys Pro Ala Leu Val Ala Val Arg Asn Glu Ser Leu Ile Asn Glu Leu

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Lys Glu Ala Leu Ala Asp Leu Asp Tyr Lys Leu Glu Ile Ile Pro Gly

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Glu Gln Gly Val Ile Glu Val Ala Arg His Pro Glu Ala Val Thr Val
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5 Val Thr Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala
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10 Ile Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile
 195 200 205

15 Ala Gly Gly Pro Phe Val Leu Pro Leu Ala Asn Lys His Asn Val Lys
 210 215 220

20 Ile Leu Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln
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Gly Leu Pro Glu Gly Ala Leu Arg Lys Ile Ile Leu Thr Ala Ser Gly
 245 250 255

25 Gly Ala Phe Arg Asp Trp Pro Val Glu Lys Leu Lys Glu Val Lys Val
 260 265 270

30 Ala Asp Ala Leu Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr
 275 280 285

35 Val Asp Ser Ala Thr Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala
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40 His Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His
 305 310 315 320

Pro Gln Ser Ile Ile His Ser Met Ile Glu Thr Gln Asp Ser Ser Val
 325 330 335

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Leu Ala Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr
 340 345 350

5 Met Ser Trp Pro Asp Arg Val Pro Cys Ser Glu Val Thr Trp Pro Arg
 355 360 365

10 Leu Asp Leu Cys Lys Leu Gly Ser Leu Thr Phe Lys Lys Pro Asp Asn
 370 375 380

15 Val Lys Tyr Pro Ser Met Asp Leu Ala Tyr Ala Ala Gly Arg Ala Gly
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Gly Thr Met Thr Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu
 405 410 415

20 Met Phe Ile Asp Glu Lys Ile Ser Tyr Leu Asp Ile Phe Lys Val Val
 420 425 430

25 Glu Leu Thr Cys Asp Lys His Arg Asn Glu Leu Val Thr Ser Pro Ser
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cttccatcac taacagtcct cgccgagggt tgaatcggtt gttcgcctca acgtcgact 179

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atg ggt gaa gtc gct gat gct ggt atg gat gcc gtc cag aag cgg ctt 227

Met Gly Glu Val Ala Asp Ala Gly Met Asp Ala Val Gln Lys Arg Leu

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atg ttc gac gat gaa tgt att ttg gtg gat gag aat gac aag gtc gtc 275

Met Phe Asp Asp Glu Cys Ile Leu Val Asp Glu Asn Asp Lys Val Val

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gga cat gat tcc aaa tac aac tgt cat ttg atg gaa aag ata gag gca 323

Gly His Asp Ser Lys Tyr Asn Cys His Leu Met Glu Lys Ile Glu Ala

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gaa aac ttg ctt cac aga gcc ttc agt gtt ttc tta ttc aac tca aaa 371

Glu Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe Asn Ser Lys

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tac gag ttg ctt ctt cag caa cga tct gca acg aag gta aca ttc ccg 419

Tyr Glu Leu Leu Leu Gln Gln Arg Ser Ala Thr Lys Val Thr Phe Pro

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ctc gta tgg aca aac acc tgt tgc agc cat ccc ctc ttc cgt gat tcc 467

Leu Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu Phe Arg Asp Ser

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95

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gaa ctc ata gaa gaa aat ttt ctc ggg gta cga aac gct gca caa agg 515

Glu Leu Ile Glu Glu Asn Phe Leu Gly Val Arg Asn Ala Ala Gln Arg

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	Lys Leu Leu Asp Glu Leu Gly Ile Pro Ala Glu Asp Val Pro Val Asp			
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	gaa ttc act cct ctt ggt cgc att ctt tac aaa gct cca tct gac gga			611
	Glu Phe Thr Pro Leu Gly Arg Ile Leu Tyr Lys Ala Pro Ser Asp Gly			
	130	135	140	
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	aaa tgg gga gag cac gaa ctg gac tat ctt ctg ttt att gtc cga gat			659
	Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile Val Arg Asp			
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	Val Lys Tyr Asp Pro Asn Pro Asp Glu Val Ala Asp Ala Lys Tyr Val			
		165	170	175
	aat cgc gag gag ttg aaa gag ata ctg aga aaa gct gat gca ggt gaa			755
20	Asn Arg Glu Glu Leu Lys Glu Ile Leu Arg Lys Ala Asp Ala Gly Glu			
		180	185	190
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	Glu Gly Ile Lys Leu Ser Pro Trp Phe Arg Leu Val Val Asp Asn Phe			
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	Leu Phe Lys Trp Trp Asp His Val Glu Glu Gly Lys Ile Lys Asp Val			
	210	215	220	
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 35 40 45
 15 Glu Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe Asn Ser Lys
 50 55 60
 20 Tyr Glu Leu Leu Leu Gln Gln Arg Ser Ala Thr Lys Val Thr Phe Pro
 65 70 75 80
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 85 90 95
 25 Glu Leu Ile Glu Glu Asn Phe Leu Gly Val Arg Asn Ala Ala Gln Arg
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 30 Lys Leu Leu Asp Glu Leu Gly Ile Pro Ala Glu Asp Val Pro Val Asp
 115 120 125
 35 Glu Phe Thr Pro Leu Gly Arg Ile Leu Tyr Lys Ala Pro Ser Asp Gly
 130 135 140
 Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile Val Arg Asp
 40 145 150 155 160
 Val Lys Tyr Asp Pro Asn Pro Asp Glu Val Ala Asp Ala Lys Tyr Val
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176

Asn Arg Glu Glu Leu Lys Glu Ile Leu Arg Lys Ala Asp Ala Gly Glu
 180 185 190

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Glu Gly Ile Lys Leu Ser Pro Trp Phe Arg Leu Val Val Asp Asn Phe
 195 200 205

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Leu Phe Lys Trp Trp Asp His Val Glu Glu Gly Lys Ile Lys Asp Val
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Ala Asp Met Lys Thr Ile His Lys Leu Thr
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5	att ccc gat cag ggt cac tct tgt tct gac tct cca cac aag ggt tac	201
	Ile Pro Asp Gln Gly His Ser Cys Ser Asp Ser Pro His Lys Gly Tyr	
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	Val Cys Arg Thr Thr Tyr Ser Leu Lys Ser Pro Val Phe Gly Gly Phe	
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15	agt cat caa ctc tat cac cag agt agc tcc ttg gtt gag gag gag ctt	297
	Ser His Gln Leu Tyr His Gln Ser Ser Ser Leu Val Glu Glu Glu Leu	
	70 75 80	
20	gac cca ttt tcg ctt gtt gcc gat gag ctg tca ctt ctt agt aat aag	345
	Asp Pro Phe Ser Leu Val Ala Asp Glu Leu Ser Leu Leu Ser Asn Lys	
	85 90 95	
25	ttg aga gag atg gta ctt gcc gag gtt cca aag ctt gcc tct gct gct	393
	Leu Arg Glu Met Val Leu Ala Glu Val Pro Lys Leu Ala Ser Ala Ala	
	100 105 110	
30	gag tac ttc ttc aaa agg ggt gtg caa gga aaa cag ttt cgt tca act	441
	Glu Tyr Phe Phe Lys Arg Gly Val Gln Gly Lys Gln Phe Arg Ser Thr	
	115 120 125 130	
35	att ttg ctg ctg atg gcg aca gct ctg gat gta cga gtt cca gaa gca	489
	Ile Leu Leu Leu Met Ala Thr Ala Leu Asp Val Arg Val Pro Glu Ala	
	135 140 145	
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	Leu Ile Gly Glu Ser Thr Asp Ile Val Thr Ser Glu Leu Arg Val Arg	
	150 155 160	
45	caa cgg ggt att gct gaa atc act gaa atg ata cac gtc gca agt cta	585
	Gln Arg Gly Ile Ala Glu Ile Thr Glu Met Ile His Val Ala Ser Leu	
	165 170 175	
50	ctg cac gat gat gtc ttg gat gat gcc gat aca agg cgt ggt gtt ggt	633
	Leu His Asp Asp Val Leu Asp Asp Ala Asp Thr Arg Arg Gly Val Gly	
	180 185 190	

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	Phe Leu Leu Ser Arg Ala Cys Gly Ala Leu Ala Ala Leu Lys Asn Thr	
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10	gag gtt gta gca tta ctt gca act gct gta gaa cat ctt gtt acc ggt	777
	Glu Val Val Ala Leu Leu Ala Thr Ala Val Glu His Leu Val Thr Gly	
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15	gaa acc atg gag ata act agt tca acc gag cag cgt tat agt atg gac	825
	Glu Thr Met Glu Ile Thr Ser Ser Thr Glu Gln Arg Tyr Ser Met Asp	
	245 250 255	
20	tac tac atg cag aag aca tat tat aag aca gca tcg cta atc tct aac	873
	Tyr Tyr Met Gln Lys Thr Tyr Tyr Lys Thr Ala Ser Leu Ile Ser Asn	
	260 265 270	
	agc tgc aaa gct ggt gcc gtt ctc act gga caa aca gca gaa gtt gcc	921
	Ser Cys Lys Ala Val Ala Val Leu Thr Gly Gln Thr Ala Glu Val Ala	
	275 280 285 290	
25	gtg tta gct ttt gag tat ggg agg aat ctg ggt tta gca ttc caa tta	969
	Val Leu Ala Phe Glu Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gln Leu	
	295 300 305	
30	ata gac gac att ctt gat ttc acg ggc aca tct gcc tct ctc gga aag	1017
	Ile Asp Asp Ile Leu Asp Phe Thr Gly Thr Ser Ala Ser Leu Gly Lys	
	310 315 320	
35	gga tcg ttg tca gat att cgc cat gga gtc ata aca gcc cca atc ctc	1065
	Gly Ser Leu Ser Asp Ile Arg His Gly Val Ile Thr Ala Pro Ile Leu	
	325 330 335	
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	Phe Ala Met Glu Glu Phe Pro Gln Leu Arg Glu Val Val Asp Gln Val	
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	gaa aaa gat cct agg aat gtt gac att gct tta gag tat ctt ggg aag	1161
	Glu Lys Asp Pro Arg Asn Val Asp Ile Ala Leu Glu Tyr Leu Gly Lys	
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45	agc aag gga ata cag agg gca aga gaa tta gcc atg gaa cat gcg aat	1209

179

Ser Lys Gly Ile Gln Arg Ala Arg Glu Leu Ala Met Glu His Ala Asn
 375 380 385

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acc aga aac aag tgagattaag taatgtttct ctctatacac caaaacattc 1357
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Ala Ile Ile Pro Asp Gln Gly His Ser Cys Ser Asp Ser Pro His Lys
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Gly Tyr Val Cys Arg Thr Thr Tyr Ser Leu Lys Ser Pro Val Phe Gly
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Gly Phe Ser His Gln Leu Tyr His Gln Ser Ser Ser Leu Val Glu Glu
 65 70 75 80

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Glu Leu Asp Pro Phe Ser Leu Val Ala Asp Glu Leu Ser Leu Leu Ser
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Ser Thr Ile Leu Leu Leu Met Ala Thr Ala Leu Asp Val Arg Val Pro
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Glu Ala Leu Ile Gly Glu Ser Thr Asp Ile Val Thr Ser Glu Leu Arg
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Val Arg Gln Arg Gly Ile Ala Glu Ile Thr Glu Met Ile His Val Ala
 165 170 175

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Ser Leu Leu His Asp Asp Val Leu Asp Asp Ala Asp Thr Arg Arg Gly
 180 185 190

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Val Gly Ser Leu Asn Val Val Met Gly Asn Lys Met Ser Val Leu Ala
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Gly Asp Phe Leu Leu Ser Arg Ala Cys Gly Ala Leu Ala Ala Leu Lys
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Asn Thr Glu Val Val Ala Leu Leu Ala Thr Ala Val Glu His Leu Val
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181

Thr Gly Glu Thr Met Glu Ile Thr Ser Ser Thr Glu Gln Arg Tyr Ser
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5 Met Asp Tyr Tyr Met Gln Lys Thr Tyr Tyr Lys Thr Ala Ser Leu Ile
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Gln Leu Ile Asp Asp Ile Leu Asp Phe Thr Gly Thr Ser Ala Ser Leu
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20 Gly Lys Gly Ser Leu Ser Asp Ile Arg His Gly Val Ile Thr Ala Pro
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30 Gln Val Glu Lys Asp Pro Arg Asn Val Asp Ile Ala Leu Glu Tyr Leu
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35 Gly Lys Ser Lys Gly Ile Gln Arg Ala Arg Glu Leu Ala Met Glu His
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 Tyr Arg Arg Arg Ile Gln Ser Ser Ser Met Glu Thr Asp Leu Lys Ser
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 Thr Phe Leu Asn Val Tyr Ser Val Leu Lys Ser Asp Leu Leu His Asp
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 Pro Ser Phe Glu Phe Thr Asn Glu Ser Arg Leu Trp Val Asp Arg Met
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 45 ctg gac tac aat gta cgt gga ggg aaa ctc aat cgg ggt ctc tct gtt 288

183

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	Val	Asp	Ser	Phe	Lys	Leu	Leu	Lys	Gln	Gly	Asn	Asp	Leu	Thr	Glu	Gln	
				100					105					110			
10	gag	ggt	ttc	ctc	tct	tgt	gct	ctc	ggg	tgg	tgc	att	gaa	tgg	ctc	caa	384
	Glu	Val	Phe	Leu	Ser	Cys	Ala	Leu	Gly	Trp	Cys	Ile	Glu	Trp	Leu	Gln	
				115				120					125				
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	Ala	Tyr	Phe	Leu	Val	Leu	Asp	Asp	Ile	Met	Asp	Asn	Ser	Val	Thr	Arg	
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	Arg	Gly	Gln	Pro	Cys	Trp	Phe	Arg	Val	Pro	Gln	Val	Gly	Met	Val	Ala	
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	Ile	Asn	Asp	Gly	Ile	Leu	Leu	Arg	Asn	His	Ile	His	Arg	Ile	Leu	Lys	
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	Lys	His	Phe	Arg	Asp	Lys	Pro	Tyr	Tyr	Val	Asp	Leu	Val	Asp	Leu	Phe	
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35	aat	gag	ggt	gag	ttg	caa	aca	gct	tgt	ggc	cag	atg	ata	gat	ttg	atc	624
	Asn	Glu	Val	Glu	Leu	Gln	Thr	Ala	Cys	Gly	Gln	Met	Ile	Asp	Leu	Ile	
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	Thr	Thr	Phe	Glu	Gly	Glu	Lys	Asp	Leu	Ala	Lys	Tyr	Ser	Leu	Ser	Ile	
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45	cac	cgt	cgt	att	gtc	cag	tac	aaa	acg	gct	tat	tac	tca	ttt	tat	ctc	720
	His	Arg	Arg	Ile	Val	Gln	Tyr	Lys	Thr	Ala	Tyr	Tyr	Ser	Phe	Tyr	Leu	
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	Pro	Val	Ala	Cys	Ala	Leu	Leu	Met	Ala	Gly	Glu	Asn	Leu	Glu	Asn	His	
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55	att	gac	gtg	aaa	aat	ggt	ctt	ggt	gac	atg	gga	atc	tac	ttc	caa	gtg	816
	Ile	Asp	Val	Lys	Asn	Val	Leu	Val	Asp	Met	Gly	Ile	Tyr	Phe	Gln	Val	

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	Gln Asp Asp Tyr Leu Asp Cys Phe Ala Asp Pro Glu Thr Leu Gly Lys			
5	275	280	285	
	ata gga aca gat ata gaa gat ttc aaa tgc tcg tgg ttg gtg gtt aag			912
	Ile Gly Thr Asp Ile Glu Asp Phe Lys Cys Ser Trp Leu Val Val Lys			
	290	295	300	
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	Ala Leu Glu Arg Cys Ser Glu Glu Gln Thr Lys Ile Leu Tyr Glu Asn			
	305	310	315	320
15	tat ggt aaa ccc gac cca tcg aac gtt gct aaa gtg aag gat ctc tac			1008
	Tyr Gly Lys Pro Asp Pro Ser Asn Val Ala Lys Val Lys Asp Leu Tyr			
	325	330	335	
	aaa gag ctg gat ctt gag gga gtt ttc atg gag tat gag agc aaa agc			1056
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	340	345	350	
	tac gag aag ctg act gga gcg att gag gga cac caa agt aaa gca atc			1104
	Tyr Glu Lys Leu Thr Gly Ala Ile Glu Gly His Gln Ser Lys Ala Ile			
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	caa gca gtg cta aaa tcc ttc ttg gct aag atc tac aag agg cag aag			1152
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5	Ala	Ile	Pro	Ser	His	His	Leu	His	Leu	Arg	Ser	Leu	Gly	Gly	Ser	Leu
					20				25					30		
10	Tyr	Arg	Arg	Arg	Ile	Gln	Ser	Ser	Ser	Met	Glu	Thr	Asp	Leu	Lys	Ser
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15	Thr	Phe	Leu	Asn	Val	Tyr	Ser	Val	Leu	Lys	Ser	Asp	Leu	Leu	His	Asp
		50					55					60				
20	Pro	Ser	Phe	Glu	Phe	Thr	Asn	Glu	Ser	Arg	Leu	Trp	Val	Asp	Arg	Met
	65					70					75				80	
25	Leu	Asp	Tyr	Asn	Val	Arg	Gly	Gly	Lys	Leu	Asn	Arg	Gly	Leu	Ser	Val
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30	Val	Asp	Ser	Phe	Lys	Leu	Leu	Lys	Gln	Gly	Asn	Asp	Leu	Thr	Glu	Gln
					100				105					110		
35	Glu	Val	Phe	Leu	Ser	Cys	Ala	Leu	Gly	Trp	Cys	Ile	Glu	Trp	Leu	Gln
					115				120					125		
40	Ala	Tyr	Phe	Leu	Val	Leu	Asp	Asp	Ile	Met	Asp	Asn	Ser	Val	Thr	Arg
		130					135					140				
45	Arg	Gly	Gln	Pro	Cys	Trp	Phe	Arg	Val	Pro	Gln	Val	Gly	Met	Val	Ala
	145					150					155				160	
50	Ile	Asn	Asp	Gly	Ile	Leu	Leu	Arg	Asn	His	Ile	His	Arg	Ile	Leu	Lys
					165					170					175	
55	Lys	His	Phe	Arg	Asp	Lys	Pro	Tyr	Tyr	Val	Asp	Leu	Val	Asp	Leu	Phe

5	Asn	Glu	Val	Glu	Leu	Gln	Thr	Ala	Cys	Gly	Gln	Met	Ile	Asp	Leu	Ile	195	200	205
10	Thr	Thr	Phe	Glu	Gly	Glu	Lys	Asp	Leu	Ala	Lys	Tyr	Ser	Leu	Ser	Ile	210	215	220
15	His	Arg	Arg	Ile	Val	Gln	Tyr	Lys	Thr	Ala	Tyr	Tyr	Ser	Phe	Tyr	Leu	225	230	235 240
20	Pro	Val	Ala	Cys	Ala	Leu	Leu	Met	Ala	Gly	Glu	Asn	Leu	Glu	Asn	His	245	250	255
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30	Gln	Asp	Asp	Tyr	Leu	Asp	Cys	Phe	Ala	Asp	Pro	Glu	Thr	Leu	Gly	Lys	275	280	285
35	Ile	Gly	Thr	Asp	Ile	Glu	Asp	Phe	Lys	Cys	Ser	Trp	Leu	Val	Val	Lys	290	295	300
40	Ala	Leu	Glu	Arg	Cys	Ser	Glu	Glu	Gln	Thr	Lys	Ile	Leu	Tyr	Glu	Asn	305	310	315 320
45	Tyr	Gly	Lys	Pro	Asp	Pro	Ser	Asn	Val	Ala	Lys	Val	Lys	Asp	Leu	Tyr	325	330	335
50	Lys	Glu	Leu	Asp	Leu	Glu	Gly	Val	Phe	Met	Glu	Tyr	Glu	Ser	Lys	Ser	340	345	350
55	Tyr	Glu	Lys	Leu	Thr	Gly	Ala	Ile	Glu	Gly	His	Gln	Ser	Lys	Ala	Ile	355	360	365

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cat cct tca act atc tta acc caa tcc aga tcc aga tct cct cct tct 96
 His Pro Ser Thr Ile Leu Thr Gln Ser Arg Ser Arg Ser Pro Pro Ser
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ctc atc acc ctt aaa ccc atc tcc ctc act cca aaa cgc acc gtt tcg 144
 Leu Ile Thr Leu Lys Pro Ile Ser Leu Thr Pro Lys Arg Thr Val Ser
 35 40 45

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tct tct tcc tcc tct tcc ctc atc acc aaa gaa gac aac aac ctc aaa 192
 Ser Ser Ser Ser Ser Ser Leu Ile Thr Lys Glu Asp Asn Asn Leu Lys
 50 55 60

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tcc tct tcc tct tcc ttc gat ttc atg tct tac atc atc cgc aaa gcc 240
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Asp Ser Val Asn Lys Ala Leu Asp Ser Ala Val Pro Leu Arg Glu Pro				
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ctc aag atc cac gaa gcg atg cgt tac tct ctc ctc gcc gga gga aaa				336
Leu Lys Ile His Glu Ala Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys				
	100	105	110	
10				
cgc gtc aga cca gtt ctc tgc atc gcc gcg tgc gag cta gtc gga gga				384
Arg Val Arg Pro Val Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly				
	115	120	125	
15				
gaa gag tct tta gct atg ccg gcg cgt tgc gcc gtg gaa atg atc cac				432
Glu Glu Ser Leu Ala Met Pro Ala Arg Cys Ala Val Glu Met Ile His				
	130	135	140	
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acc atg tcg ttg atc cac gac gac ttg cct tgt atg gat aac gac gat				480
Thr Met Ser Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp				
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Ala Val Leu Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Leu				
	180	185	190	
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gcg tcg gct acg agc tcg gag gtt tct ccg gcg aga gtg gtt aga gct				624
Ala Ser Ala Thr Ser Ser Glu Val Ser Pro Ala Arg Val Val Arg Ala				
	195	200	205	
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gtg gga gag ttg gct aaa gcc atc ggc acc gaa ggg ctc gtg gcg gga				672
Val Gly Glu Leu Ala Lys Ala Ile Gly Thr Glu Gly Leu Val Ala Gly				
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Leu Glu His Leu Lys Phe Ile His Leu His Lys Thr Ala Ala Leu Leu				
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	Glu Ile Glu Arg Leu Arg Lys Phe Ala Arg Cys Ile Gly Leu Leu Phe	
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	cag gtg gtt gat gat atc ttg gac gtg acg aaa tcg tct caa gaa ctg	912
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	Gly Lys Thr Ala Gly Lys Asp Leu Ile Ala Asp Lys Leu Thr Tyr Pro	
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15 Ser Ser Ser Ser Ser Phe Asp Phe Met Ser Tyr Ile Ile Arg Lys Ala
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 85 90 95

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Arg Val Arg Pro Val Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly
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30 Glu Glu Ser Leu Ala Met Pro Ala Arg Cys Ala Val Glu Met Ile His
 130 135 140

35 Thr Met Ser Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp
 145 150 155 160

40 Leu Arg Arg Gly Lys Pro Thr Asn His Lys Val Tyr Gly Glu Asp Val
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 Val Ile Asp Asp Gln Thr Leu Gly Phe Gln Ala Arg Gln Pro Ala Leu
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 caa acg ccc gaa caa cgt ctg atg caa ctt gag atg aaa acg cgc cag 240
 Gln Thr Pro Glu Gln Arg Leu Met Gln Leu Glu Met Lys Thr Arg Gln
 65 70 75 80
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193

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	Asp Asp Thr Leu Arg Tyr Cys Tyr His Val Ala Gly Val Val Gly Leu	
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	165 170 175	
	att gtg gac gat gcg cat gcg ggc cgc tgt tat ctg ccg gca agc tgg	576
	Ile Val Asp Asp Ala His Ala Gly Arg Cys Tyr Leu Pro Ala Ser Trp	
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	Arg Gln Ala Leu Ser Arg Ile Ala Arg Arg Leu Val Gln Glu Ala Glu	
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194

Thr Thr Thr Pro Glu Lys Leu Thr Leu Leu Leu Ala Ala Ser Gly Gln
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 50 55 60

40 Gln Thr Pro Glu Gln Arg Leu Met Gln Leu Glu Met Lys Thr Arg Gln
 65 70 75 80

45 Ala Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala Ala Phe Gln

195

85

90

95

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			115						120					125			
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	Asp	Asp	Thr	Leu	Arg	Tyr	Cys	Tyr	His	Val	Ala	Gly	Val	Val	Gly	Leu	
		130					135						140				
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		210					215					220					
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	225					230					235					240	
40																	
	Ser	Ala	Trp	Ala	Ile	Ala	Thr	Ala	Lys	Gln	Val	Tyr	Arg	Lys	Ile	Gly	
					245					250					255		
	Val	Lys	Val	Glu	Gln	Ala	Gly	Gln	Gln	Ala	Trp	Asp	Gln	Arg	Gln	Ser	
45				260					265						270		

Thr Thr Thr Pro Glu Lys Leu Thr Leu Leu Leu Ala Ala Ser Gly Gln
 275 280 285
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Ala Leu Thr Ser Arg Met Arg Ala His Pro Pro Arg Pro Ala His Leu
 290 295 300

10 Trp Gln Arg Pro Leu
 305

15 <210> 117
 <211> 1479
 <212> DNA
 20 <213> Erwinia ureidovorana

25 <220>
 <221> CDS
 <222> (1)..(1479)
 30 <223>

35 <400> 117
 atg aaa cca act acg gta att ggt gca ggc ttc ggt ggc ctg gca ctg 48
 Met Lys Pro Thr Thr Val Ile Gly Ala Gly Phe Gly Gly Leu Ala Leu
 1 5 10 15

40 gca att cgt cta caa gct gcg ggg atc ccc gtc tta ctg ctt gaa caa 96
 Ala Ile Arg Leu Gln Ala Ala Gly Ile Pro Val Leu Leu Leu Glu Gln
 20 25 30

45 cgt gat aaa ccc ggc ggt cgg gct tat gtc tac gag gat cag ggg ttt 144
 Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Glu Asp Gln Gly Phe

	35	40	45	
	acc ttt gat gca ggc ccg acg gtt atc acc gat ccc agt gcc att gaa	192		
	Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu			
5	50	55	60	
	gaa ctg ttt gca ctg gca gga aaa cag tta aaa gag tat gtc gaa ctg	240		
	Glu Leu Phe Ala Leu Ala Gly Lys Gln Leu Lys Glu Tyr Val Glu Leu			
	65	70	75	80
10				
	ctg ccg gtt acg ccg ttt tac cgc ctg tgt tgg gag tca ggg aag gtc	288		
	Leu Pro Val Thr Pro Phe Tyr Arg Leu Cys Trp Glu Ser Gly Lys Val			
		85	90	95
15				
	ttt aat tac gat aac gat caa acc cgg ctc gaa gcg cag att cag cag	336		
	Phe Asn Tyr Asp Asn Asp Gln Thr Arg Leu Glu Ala Gln Ile Gln Gln			
		100	105	110
	ttt aat ccc cgc gat gtc gaa ggt tat cgt cag ttt ctg gac tat tca	384		
20	Phe Asn Pro Arg Asp Val Glu Gly Tyr Arg Gln Phe Leu Asp Tyr Ser			
		115	120	125
	cgc gcg gtg ttt aaa gaa ggc tat cta aag ctc ggt act gtc cct ttt	432		
	Arg Ala Val Phe Lys Glu Gly Tyr Leu Lys Leu Gly Thr Val Pro Phe			
25	130	135	140	
	tta tcg ttc aga gac atg ctt cgc gcc gca cct caa ctg gcg aaa ctg	480		
	Leu Ser Phe Arg Asp Met Leu Arg Ala Ala Pro Gln Leu Ala Lys Leu			
	145	150	155	160
30				
	cag gca tgg aga agc gtt tac agt aag gtt gcc agt tac atc gaa gat	528		
	Gln Ala Trp Arg Ser Val Tyr Ser Lys Val Ala Ser Tyr Ile Glu Asp			
		165	170	175
35				
	gaa cat ctg cgc cag gcg ttt tct ttc cac tcg ctg ttg gtg ggc ggc	576		
	Glu His Leu Arg Gln Ala Phe Ser Phe His Ser Leu Leu Val Gly Gly			
		180	185	190
	aat ccc ttc gcc acc tca tcc att tat acg ttg ata cac gcg ctg gag	624		
40	Asn Pro Phe Ala Thr Ser Ser Ile Tyr Thr Leu Ile His Ala Leu Glu			
		195	200	205
	cgt gag tgg ggc gtc tgg ttt ccg cgt ggc ggc acc ggc gca tta gtt	672		
	Arg Glu Trp Gly Val Trp Phe Pro Arg Gly Gly Thr Gly Ala Leu Val			
45	210	215	220	

	cag ggg atg ata aag ctg ttt cag gat ctg ggt ggc gaa gtc gtg tta Gln Gly Met Ile Lys Leu Phe Gln Asp Leu Gly Gly Glu Val Val Leu 225 230 235 240	720
5	aac gcc aga gtc agc cat atg gaa acg aca gga aac aag att gaa gcc Asn Ala Arg Val Ser His Met Glu Thr Thr Gly Asn Lys Ile Glu Ala 245 250 255	768
10	gtg cat tta gag gac ggt cgc agg ttc ctg acg caa gcc gtc gcg tca Val His Leu Glu Asp Gly Arg Arg Phe Leu Thr Gln Ala Val Ala Ser 260 265 270	816
15	aat gca gat gtg gtt cat acc tat cgc gac ctg tta agc cag cac cct Asn Ala Asp Val Val His Thr Tyr Arg Asp Leu Leu Ser Gln His Pro 275 280 285	864
20	gcc gcg gtt aag cag tcc aac aaa ctg cag act aag cgc atg agt aac Ala Ala Val Lys Gln Ser Asn Lys Leu Gln Thr Lys Arg Met Ser Asn 290 295 300	912
25	tct ctg ttt gtg ctc tat ttt ggt ttg aat cac cat cat gat cag ctc Ser Leu Phe Val Leu Tyr Phe Gly Leu Asn His His His Asp Gln Leu 305 310 315 320	960
	gcg cat cac acg gtt tgt ttc ggc ccg cgt tac cgc gag ctg att gac Ala His His Thr Val Cys Phe Gly Pro Arg Tyr Arg Glu Leu Ile Asp 325 330 335	1008
30	gaa att ttt aat cat gat ggc ctc gca gag gac ttc tca ctt tat ctg Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp Phe Ser Leu Tyr Leu 340 345 350	1056
35	cac gcg ccc tgt gtc acg gat tcg tca ctg gcg cct gaa ggt tgc ggc His Ala Pro Cys Val Thr Asp Ser Ser Leu Ala Pro Glu Gly Cys Gly 355 360 365	1104
40	agt tac tat gtg ttg gcg ccg gtg ccg cat tta ggc acc gcg aac ctc Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu Gly Thr Ala Asn Leu 370 375 380	1152
45	gac tgg acg gtt gag ggg cca aaa cta cgc gac cgt att ttt gcg tac Asp Trp Thr Val Glu Gly Pro Lys Leu Arg Asp Arg Ile Phe Ala Tyr 385 390 395 400	1200

ctt gag cag cat tac atg cct ggc tta cgg agt cag ctg gtc acg cac 1248
 Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser Gln Leu Val Thr His
 405 410 415

5 cgg atg ttt acg ccg ttt gat ttt cgc gac cag ctt aat gcc tat cat 1296
 Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Gln Leu Asn Ala Tyr His
 420 425 430

10 ggc tca gcc ttt tct gtg gag ccc gtt ctt acc cag agc gcc tgg ttt 1344
 Gly Ser Ala Phe Ser Val Glu Pro Val Leu Thr Gln Ser Ala Trp Phe
 435 440 445

15 cgg ccg cat aac cgc gat aaa acc att act aat ctc tac ctg gtc ggc 1392
 Arg Pro His Asn Arg Asp Lys Thr Ile Thr Asn Leu Tyr Leu Val Gly
 450 455 460

20 gca ggc acg cat ccc ggc gca ggc att cct ggc gtc atc ggc tcg gca 1440
 Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly Val Ile Gly Ser Ala
 465 470 475 480

aaa gcg aca gca ggt ttg atg ctg gag gat ctg ata tga 1479
 Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu Ile
 485 490

25
 <210> 118
 <211> 492

30 <212> PRT
 <213> Erwinia uredovora

35
 <400> 118

Met Lys Pro Thr Thr Val Ile Gly Ala Gly Phe Gly Gly Leu Ala Leu
 1 5 10 15

40
 Ala Ile Arg Leu Gln Ala Ala Gly Ile Pro Val Leu Leu Leu Glu Gln
 20 25 30

45

200

Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Glu Asp Gln Gly Phe
 35 40 45

5 Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu
 50 55 60

10 Glu Leu Phe Ala Leu Ala Gly Lys Gln Leu Lys Glu Tyr Val Glu Leu
 65 70 75 80

15 Leu Pro Val Thr Pro Phe Tyr Arg Leu Cys Trp Glu Ser Gly Lys Val
 85 90 95

Phe Asn Tyr Asp Asn Asp Gln Thr Arg Leu Glu Ala Gln Ile Gln Gln
 100 105 110

20 Phe Asn Pro Arg Asp Val Glu Gly Tyr Arg Gln Phe Leu Asp Tyr Ser
 115 120 125

25 Arg Ala Val Phe Lys Glu Gly Tyr Leu Lys Leu Gly Thr Val Pro Phe
 130 135 140

30 Leu Ser Phe Arg Asp Met Leu Arg Ala Ala Pro Gln Leu Ala Lys Leu
 145 150 155 160

35 Gln Ala Trp Arg Ser Val Tyr Ser Lys Val Ala Ser Tyr Ile Glu Asp
 165 170 175

40 Glu His Leu Arg Gln Ala Phe Ser Phe His Ser Leu Leu Val Gly Gly
 180 185 190

45 Asn Pro Phe Ala Thr Ser Ser Ile Tyr Thr Leu Ile His Ala Leu Glu
 195 200 205

Arg Glu Trp Gly Val Trp Phe Pro Arg Gly Gly Thr Gly Ala Leu Val

	210		215		220
5	Gln Gly Met Ile Lys Leu Phe Gln Asp Leu Gly Gly Glu Val Val Leu				
	225		230		235 240
10	Asn Ala Arg Val Ser His Met Glu Thr Thr Gly Asn Lys Ile Glu Ala				
		245		250	255
	Val His Leu Glu Asp Gly Arg Arg Phe Leu Thr Gln Ala Val Ala Ser				
		260		265	270
15	Asn Ala Asp Val Val His Thr Tyr Arg Asp Leu Leu Ser Gln His Pro				
		275		280	285
20	Ala Ala Val Lys Gln Ser Asn Lys Leu Gln Thr Lys Arg Met Ser Asn				
		290		295	300
25	Ser Leu Phe Val Leu Tyr Phe Gly Leu Asn His His His Asp Gln Leu				
		305		310 315	320
30	Ala His His Thr Val Cys Phe Gly Pro Arg Tyr Arg Glu Leu Ile Asp				
		325		330	335
	Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp Phe Ser Leu Tyr Leu				
		340		345	350
35	His Ala Pro Cys Val Thr Asp Ser Ser Leu Ala Pro Glu Gly Cys Gly				
		355		360	365
40	Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu Gly Thr Ala Asn Leu				
		370		375	380
45	Asp Trp Thr Val Glu Gly Pro Lys Leu Arg Asp Arg Ile Phe Ala Tyr				
		385		390 395	400

Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser Gln Leu Val Thr His
405 410 415

5

Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Gln Leu Asn Ala Tyr His
420 425 430

10

Gly Ser Ala Phe Ser Val Glu Pro Val Leu Thr Gln Ser Ala Trp Phe
435 440 445

15

Arg Pro His Asn Arg Asp Lys Thr Ile Thr Asn Leu Tyr Leu Val Gly
450 455 460

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Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly Val Ile Gly Ser Ala
465 470 475 480

Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu Ile
485 490

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<210> 119

<211> 1725

30

<212> DNA

<213> Narcissus pseudonarcissus

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<220>

<221> CDS

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<222> (1)..(1725)

<223>

<400> 119

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1 5 10 15

10 gga aag aaa gtg aag atg aac acg atg att cga tgc aag ttg ttt tca 96
Gly Lys Lys Val Lys Met Asn Thr Met Ile Arg Ser Lys Leu Phe Ser
20 25 30

15 att cgg tgc gct ttg gac act aag gtg tct gat atg agc gtc aat gct 144
Ile Arg Ser Ala Leu Asp Thr Lys Val Ser Asp Met Ser Val Asn Ala
35 40 45

cca aaa gga ttg ttt cca cca gag cct gag cac tac agg ggg cca aag 192
Pro Lys Gly Leu Phe Pro Pro Glu Pro Glu His Tyr Arg Gly Pro Lys
50 55 60

20 ctt aaa gtg gct atc att gga gct ggg ctc gct ggc atg tca act gca 240
Leu Lys Val Ala Ile Ile Gly Ala Gly Leu Ala Gly Met Ser Thr Ala
65 70 75 80

25 gtg gag ctt ttg gat caa ggg cat gag gtt gac ata tat gaa tcc aga 288
Val Glu Leu Leu Asp Gln Gly His Glu Val Asp Ile Tyr Glu Ser Arg
85 90 95

30 caa ttt att ggt ggt aaa gtc ggt tct ttt gta gat aag cgt gga aac 336
Gln Phe Ile Gly Gly Lys Val Gly Ser Phe Val Asp Lys Arg Gly Asn
100 105 110

35 cat att gaa atg gga ctc cat gtg ttt ttt ggt tgc tat aac aat ctt 384
His Ile Glu Met Gly Leu His Val Phe Phe Gly Cys Tyr Asn Asn Leu
115 120 125

ttc aga ctt atg aaa aag gta ggt gca gat gaa aat tta ctg gtg aag 432
Phe Arg Leu Met Lys Lys Val Gly Ala Asp Glu Asn Leu Leu Val Lys
130 135 140

40 gat cat act cat acc ttt gta aac cga ggt gga gaa att ggt gaa ctt 480
Asp His Thr His Thr Phe Val Asn Arg Gly Gly Glu Ile Gly Glu Leu
145 150 155 160

45 gat ttc cga ctt ccg atg ggt gca cca tta cat ggt att cgt gca ttt 528
Asp Phe Arg Leu Pro Met Gly Ala Pro Leu His Gly Ile Arg Ala Phe

204

	165	170	175	
	cta aca act aat caa ctg aag cct tat gat aaa gca agg aat gct gtg			576
	Leu Thr Thr Asn Gln Leu Lys Pro Tyr Asp Lys Ala Arg Asn Ala Val			
5	180	185	190	
	gct ctt gcc ctt agc cca gtt gta cgt gct ctt att gat cca aat ggt			624
	Ala Leu Ala Leu Ser Pro Val Val Arg Ala Leu Ile Asp Pro Asn Gly			
	195	200	205	
10				
	gca atg cag gat ata agg aac tta gat aat att agc ttt tct gat tgg			672
	Ala Met Gln Asp Ile Arg Asn Leu Asp Asn Ile Ser Phe Ser Asp Trp			
	210	215	220	
15				
	ttc tta tcc aaa ggc ggt acc cgc atg agc atc caa agg atg tgg gat			720
	Phe Leu Ser Lys Gly Gly Thr Arg Met Ser Ile Gln Arg Met Trp Asp			
	225	230	235	240
	cca gtt gct tat gcc ctc gga ttt att gac tgt gat aat atc agt gcc			768
20	Pro Val Ala Tyr Ala Leu Gly Phe Ile Asp Cys Asp Asn Ile Ser Ala			
	245	250	255	
	cgt tgt atg ctt act ata ttt tct cta ttt gct act aag aca gaa gct			816
	Arg Cys Met Leu Thr Ile Phe Ser Leu Phe Ala Thr Lys Thr Glu Ala			
25	260	265	270	
	tct ctg ttg cgt atg ttg aag ggt tcg cct gat gtt tac tta agc ggt			864
	Ser Leu Leu Arg Met Leu Lys Gly Ser Pro Asp Val Tyr Leu Ser Gly			
	275	280	285	
30				
	cct ata aga aag tat att aca gat aaa ggt gga agg ttt cac cta agg			912
	Pro Ile Arg Lys Tyr Ile Thr Asp Lys Gly Gly Arg Phe His Leu Arg			
	290	295	300	
35				
	tgg ggg tgt aga gag ata ctt tat gat gaa cta tca aat ggc gac aca			960
	Trp Gly Cys Arg Glu Ile Leu Tyr Asp Glu Leu Ser Asn Gly Asp Thr			
	305	310	315	320
	tat atc aca ggc att gca atg tcg aag gct acc aat aaa aaa ctt gtg			1008
40	Tyr Ile Thr Gly Ile Ala Met Ser Lys Ala Thr Asn Lys Lys Leu Val			
	325	330	335	
	aaa gct gac gtg tat gtt gca gca tgt gat gtt cct gga ata aaa agg			1056
	Lys Ala Asp Val Tyr Val Ala Ala Cys Asp Val Pro Gly Ile Lys Arg			
45	340	345	350	

	ttg atc cca tcg gag tgg aga gaa tgg gat cta ttt gac aat atc tat Leu Ile Pro Ser Glu Trp Arg Glu Trp Asp Leu Phe Asp Asn Ile Tyr 355 360 365	1104
5	aaa cta gtt gga gtt cca gtt gtc act gtt cag ctt agg tac aat ggt Lys Leu Val Gly Val Pro Val Val Thr Val Gln Leu Arg Tyr Asn Gly 370 375 380	1152
10	tgg gtg aca gag atg caa gat ctg gaa aaa tca agg cag ttg aga gct Trp Val Thr Glu Met Gln Asp Leu Glu Lys Ser Arg Gln Leu Arg Ala 385 390 395 400	1200
15	gca gta gga ttg gat aat ctt ctt tat act cca gat gca gac ttt tct Ala Val Gly Leu Asp Asn Leu Leu Tyr Thr Pro Asp Ala Asp Phe Ser 405 410 415	1248
20	tgt ttt tct gat ctt gca ctc tcg tcg cct gaa gat tat tat att gaa Cys Phe Ser Asp Leu Ala Leu Ser Ser Pro Glu Asp Tyr Tyr Ile Glu 420 425 430	1296
25	gga caa ggg tcc cta ata cag gct gtt ctc acg cca ggg gat cca tac Gly Gln Gly Ser Leu Ile Gln Ala Val Leu Thr Pro Gly Asp Pro Tyr 435 440 445	1344
	atg ccc cta cct aat gat gca att ata gaa aga gtt cgg aaa cag gtt Met Pro Leu Pro Asn Asp Ala Ile Ile Glu Arg Val Arg Lys Gln Val 450 455 460	1392
30	ttg gat tta ttc cca tcc tct caa ggc ctg gaa gtt cta tgg tct tcg Leu Asp Leu Phe Pro Ser Ser Gln Gly Leu Glu Val Leu Trp Ser Ser 465 470 475 480	1440
35	gtg gtt aaa atc gga caa tcc cta tat cgg gag ggg cct gga aag gac Val Val Lys Ile Gly Gln Ser Leu Tyr Arg Glu Gly Pro Gly Lys Asp 485 490 495	1488
40	cca ttc aga cct gat cag aag aca cca gta aaa aat ttc ttc ctt gca Pro Phe Arg Pro Asp Gln Lys Thr Pro Val Lys Asn Phe Phe Leu Ala 500 505 510	1536
45	ggg tca tac acc aaa cag gat tac att gac agt atg gaa gga gcg acc Gly Ser Tyr Thr Lys Gln Asp Tyr Ile Asp Ser Met Glu Gly Ala Thr 515 520 525	1584

206

cta tcg ggg aga caa gca gct gca tat atc tgc agc gcc ggt gaa gat 1632
 Leu Ser Gly Arg Gln Ala Ala Ala Tyr Ile Cys Ser Ala Gly Glu Asp
 530 535 540

5 ctg gca gca ctt cgc aag aag atc gct gct gat cat cca gag caa ctg 1680
 Leu Ala Ala Leu Arg Lys Lys Ile Ala Ala Asp His Pro Glu Gln Leu
 545 550 555 560

10 atc aac aaa gat tct aac gtg tcg gat gaa ctg agt ctc gta taa 1725
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 565 570

<210> 120

15 <211> 574

<212> PRT

20 <213> Narcissus pseudonarcissus

<400> 120

25 Met Ala Ser Ser Thr Cys Leu Ile His Ser Ser Ser Phe Gly Val Gly
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30 Gly Lys Lys Val Lys Met Asn Thr Met Ile Arg Ser Lys Leu Phe Ser
 20 25 30

Ile Arg Ser Ala Leu Asp Thr Lys Val Ser Asp Met Ser Val Asn Ala
 35 35 40 45

Pro Lys Gly Leu Phe Pro Pro Glu Pro Glu His Tyr Arg Gly Pro Lys
 50 55 60

40 Leu Lys Val Ala Ile Ile Gly Ala Gly Leu Ala Gly Met Ser Thr Ala
 65 70 75 80

45

207

	Val	Glu	Leu	Leu	Asp	Gln	Gly	His	Glu	Val	Asp	Ile	Tyr	Glu	Ser	Arg	
					85					90						95	
5	Gln	Phe	Ile	Gly	Gly	Lys	Val	Gly	Ser	Phe	Val	Asp	Lys	Arg	Gly	Asn	
				100					105						110		
10	His	Ile	Glu	Met	Gly	Leu	His	Val	Phe	Phe	Gly	Cys	Tyr	Asn	Asn	Leu	
				115					120						125		
15	Phe	Arg	Leu	Met	Lys	Lys	Val	Gly	Ala	Asp	Glu	Asn	Leu	Leu	Val	Lys	
				130				135						140			
20	Asp	His	Thr	His	Thr	Phe	Val	Asn	Arg	Gly	Gly	Glu	Ile	Gly	Glu	Leu	
				145				150				155				160	
25	Asp	Phe	Arg	Leu	Pro	Met	Gly	Ala	Pro	Leu	His	Gly	Ile	Arg	Ala	Phe	
					165					170					175		
30	Leu	Thr	Thr	Asn	Gln	Leu	Lys	Pro	Tyr	Asp	Lys	Ala	Arg	Asn	Ala	Val	
					180					185					190		
35	Ala	Leu	Ala	Leu	Ser	Pro	Val	Val	Arg	Ala	Leu	Ile	Asp	Pro	Asn	Gly	
					195				200					205			
40	Ala	Met	Gln	Asp	Ile	Arg	Asn	Leu	Asp	Asn	Ile	Ser	Phe	Ser	Asp	Trp	
				210				215					220				
45	Phe	Leu	Ser	Lys	Gly	Gly	Thr	Arg	Met	Ser	Ile	Gln	Arg	Met	Trp	Asp	
				225			230				235				240		
50	Pro	Val	Ala	Tyr	Ala	Leu	Gly	Phe	Ile	Asp	Cys	Asp	Asn	Ile	Ser	Ala	
					245					250					255		
55	Arg	Cys	Met	Leu	Thr	Ile	Phe	Ser	Leu	Phe	Ala	Thr	Lys	Thr	Glu	Ala	

	260	265	270
5	Ser Leu Leu Arg Met Leu Lys Gly Ser Pro Asp Val Tyr Leu Ser Gly		
	275	280	285
10	Pro Ile Arg Lys Tyr Ile Thr Asp Lys Gly Gly Arg Phe His Leu Arg		
	290	295	300
15	Trp Gly Cys Arg Glu Ile Leu Tyr Asp Glu Leu Ser Asn Gly Asp Thr		
	305	310	315 320
20	Tyr Ile Thr Gly Ile Ala Met Ser Lys Ala Thr Asn Lys Lys Leu Val		
	325	330	335
25	Lys Ala Asp Val Tyr Val Ala Ala Cys Asp Val Pro Gly Ile Lys Arg		
	340	345	350
30	Leu Ile Pro Ser Glu Trp Arg Glu Trp Asp Leu Phe Asp Asn Ile Tyr		
	355	360	365
35	Lys Leu Val Gly Val Pro Val Val Thr Val Gln Leu Arg Tyr Asn Gly		
	370	375	380
40	Trp Val Thr Glu Met Gln Asp Leu Glu Lys Ser Arg Gln Leu Arg Ala		
	385	390	395 400
45	Ala Val Gly Leu Asp Asn Leu Leu Tyr Thr Pro Asp Ala Asp Phe Ser		
	405	410	415
50	Cys Phe Ser Asp Leu Ala Leu Ser Ser Pro Glu Asp Tyr Tyr Ile Glu		
	420	425	430
55	Gly Gln Gly Ser Leu Ile Gln Ala Val Leu Thr Pro Gly Asp Pro Tyr		
	435	440	445

5 Met Pro Leu Pro Asn Asp Ala Ile Ile Glu Arg Val Arg Lys Gln Val
 450 455 460

10 Leu Asp Leu Phe Pro Ser Ser Gln Gly Leu Glu Val Leu Trp Ser Ser
 465 470 475 480

15 Val Val Lys Ile Gly Gln Ser Leu Tyr Arg Glu Gly Pro Gly Lys Asp
 485 490 495

20 Gly Ser Tyr Thr Lys Gln Asp Tyr Ile Asp Ser Met Glu Gly Ala Thr
 515 520 525

25 Leu Ser Gly Arg Gln Ala Ala Ala Tyr Ile Cys Ser Ala Gly Glu Asp
 530 535 540

30 Leu Ala Ala Leu Arg Lys Lys Ile Ala Ala Asp His Pro Glu Gln Leu
 545 550 555 560

35 Ile Asn Lys Asp Ser Asn Val Ser Asp Glu Leu Ser Leu Val
 565 570

40 <210> 121
 <211> 1848
 <212> DNA
 <213> Lycopersicon esculentum

<220>

<221> CDS

5 <222> (1)..(1848)

<223>

10

<400> 121

atg tgt acc ttg agt ttt atg tat cct aat tca ctt ctt gat ggt acc 48
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15

tgc aag act gta gct ttg ggt gat agc aaa cca aga tac aat aaa cag 96
 Cys Lys Thr Val Ala Leu Gly Asp Ser Lys Pro Arg Tyr Asn Lys Gln
 20 25 30

20

aga agt tct tgt ttt gac cct ttg ata att gga aat tgt act gat cag 144
 Arg Ser Ser Cys Phe Asp Pro Leu Ile Ile Gly Asn Cys Thr Asp Gln
 35 40 45

25

cag cag ctt tgt ggc ttg agt tgg ggg gtg gac aag gct aag gga aga 192
 Gln Gln Leu Cys Gly Leu Ser Trp Gly Val Asp Lys Ala Lys Gly Arg
 50 55 60

30

aga ggg ggt act gtt tcc aat ttg aaa gca gtt gta gat gta gac aaa 240
 Arg Gly Gly Thr Val Ser Asn Leu Lys Ala Val Val Asp Val Asp Lys
 65 70 75 80

35

aga gtg gag agc tat ggc agt agt gat gta gaa gga aat gag agt ggc 288
 Arg Val Glu Ser Tyr Gly Ser Ser Asp Val Glu Gly Asn Glu Ser Gly
 85 90 95

agc tat gat gcc att gtt ata ggt tca gga ata ggt gga ttg gtg gca 336
 Ser Tyr Asp Ala Ile Val Ile Gly Ser Gly Ile Gly Gly Leu Val Ala
 100 105 110

40

gcg acg cag ctg gcg gtt aag gga gct aag gtt tta gtt ctg gag aag 384
 Ala Thr Gln Leu Ala Val Lys Gly Ala Lys Val Leu Val Leu Glu Lys
 115 120 125

45

tat gtt att cct ggt gga agc tct ggc ttt tac gag agg gat ggt tat 432
 Tyr Val Ile Pro Gly Gly Ser Ser Gly Phe Tyr Glu Arg Asp Gly Tyr

211

	130	135	140	
	aag ttt gat gtt ggt tca tca gtg atg ttt gga ttc agt gat aag gga			480
	Lys Phe Asp Val Gly Ser Ser Val Met Phe Gly Phe Ser Asp Lys Gly			
5	145	150	155	160
	aac ctc aat tta att act caa gca ttg gca gca gta gga cgt aaa tta			528
	Asn Leu Asn Leu Ile Thr Gln Ala Leu Ala Ala Val Gly Arg Lys Leu			
		165	170	175
10				
	gaa gtt ata cct gac cca aca act gta cat ttc cac ctg cca aat gac			576
	Glu Val Ile Pro Asp Pro Thr Thr Val His Phe His Leu Pro Asn Asp			
		180	185	190
15				
	ctt tct gtt cgt ata cac cga gag tat gat gac ttc att gaa gag ctt			624
	Leu Ser Val Arg Ile His Arg Glu Tyr Asp Asp Phe Ile Glu Glu Leu			
		195	200	205
	gtg agt aaa ttt cca cat gaa aag gaa ggg att atc aaa ttt tac agt			672
20	Val Ser Lys Phe Pro His Glu Lys Glu Gly Ile Ile Lys Phe Tyr Ser			
		210	215	220
	gaa tgc tgg aag atc ttt aat tct ctg aat tca ttg gaa ctg aag tct			720
	Glu Cys Trp Lys Ile Phe Asn Ser Leu Asn Ser Leu Glu Leu Lys Ser			
25	225	230	235	240
	ttg gag gaa ccc atc tac ctt ttt ggc cag ttc ttt aag aag ccc ctt			768
	Leu Glu Glu Pro Ile Tyr Leu Phe Gly Gln Phe Phe Lys Lys Pro Leu			
		245	250	255
30				
	gaa tgc ttg act ctt gcc tac tat ttg ccc cag aat gct ggt agc atc			816
	Glu Cys Leu Thr Leu Ala Tyr Tyr Leu Pro Gln Asn Ala Gly Ser Ile			
		260	265	270
35				
	gct cgg aag tat ata aga gat cct ggg ttg ctg tct ttt ata gat gca			864
	Ala Arg Lys Tyr Ile Arg Asp Pro Gly Leu Leu Ser Phe Ile Asp Ala			
		275	280	285
	gag tgc ttt atc gtg agt aca gtt aat gca tta caa aca cca atg atc			912
40	Glu Cys Phe Ile Val Ser Thr Val Asn Ala Leu Gln Thr Pro Met Ile			
		290	295	300
	aat gca agc atg gtt cta tgt gac aga cat ttt ggc gga atc aac tac			960
	Asn Ala Ser Met Val Leu Cys Asp Arg His Phe Gly Gly Ile Asn Tyr			
45	305	310	315	320

	ccc gtt ggt gga gtt ggc gag atc gcc aaa tcc tta gca aaa ggc ttg	1008
	Pro Val Gly Gly Val Gly Glu Ile Ala Lys Ser Leu Ala Lys Gly Leu	
	325 330 335	
5		
	gat gat cac gga agt cag ata ctt tat agg gca aat gtt aca agt atc	1056
	Asp Asp His Gly Ser Gln Ile Leu Tyr Arg Ala Asn Val Thr Ser Ile	
	340 345 350	
10		
	att ttg gac aat ggc aaa gct gtg gga gtg aag ctt tct gac ggg agg	1104
	Ile Leu Asp Asn Gly Lys Ala Val Gly Val Lys Leu Ser Asp Gly Arg	
	355 360 365	
	aag ttt tat gct aaa acc ata gta tcg aat gct acc aga tgg gat act	1152
15	Lys Phe Tyr Ala Lys Thr Ile Val Ser Asn Ala Thr Arg Trp Asp Thr	
	370 375 380	
	ttt gga aag ctt tta aaa gct gag aat ctg cca aaa gaa gaa gaa aat	1200
	Phe Gly Lys Leu Leu Lys Ala Glu Asn Leu Pro Lys Glu Glu Glu Asn	
20	385 390 395 400	
	ttc cag aaa gct tat gta aaa gca cct tct ttt ctt tct att cat atg	1248
	Phe Gln Lys Ala Tyr Val Lys Ala Pro Ser Phe Leu Ser Ile His Met	
	405 410 415	
25		
	gga gtt aaa gca gat gta ctc cca cca gac aca gat tgt cac cat ttt	1296
	Gly Val Lys Ala Asp Val Leu Pro Pro Asp Thr Asp Cys His His Phe	
	420 425 430	
30		
	gtc ctc gag gat gat tgg aca aat ttg gag aaa cca tat gga agt ata	1344
	Val Leu Glu Asp Asp Trp Thr Asn Leu Glu Lys Pro Tyr Gly Ser Ile	
	435 440 445	
	ttc ttg agt att cca aca gtt ctt gat tcc tca ttg gcc cca gaa gga	1392
35	Phe Leu Ser Ile Pro Thr Val Leu Asp Ser Ser Leu Ala Pro Glu Gly	
	450 455 460	
	cac cat att ctt cac att ttt aca aca tcg agc att gaa gat tgg gag	1440
	His His Ile Leu His Ile Phe Thr Thr Ser Ser Ile Glu Asp Trp Glu	
40	465 470 475 480	
	gga ctc tct ccg aaa gac tat gaa gcg aag aaa gag gtt gtt gct gaa	1488
	Gly Leu Ser Pro Lys Asp Tyr Glu Ala Lys Lys Glu Val Val Ala Glu	
	485 490 495	
45		

213

	agg att ata agc aga ctt gaa aaa aca ctc ttc cca ggg ctt aag tca	1536
	Arg Ile, Ile Ser Arg Leu Glu Lys Thr Leu Phe Pro Gly Leu Lys Ser	
	500 505 510	
5	tct att ctc ttt aag gag gtg gga act cca aag acc cac aga cga tac	1584
	Ser Ile Leu Phe Lys Glu Val Gly Thr Pro Lys Thr His Arg Arg Tyr	
	515 520 525	
10	ctt gct cgt gat agt ggt acc tat gga cca atg cca cgc gga aca cct	1632
	Leu Ala Arg Asp Ser Gly Thr Tyr Gly Pro Met Pro Arg Gly Thr Pro	
	530 535 540	
15	aag gga ctc ctg gga atg cct ttc aat acc act gct ata gat ggt cta	1680
	Lys Gly Leu Leu Gly Met Pro Phe Asn Thr Thr Ala Ile Asp Gly Leu	
	545 550 555 560	
20	tat tgt gtt ggc gat agt tgc ttc cca gga caa ggt gtt ata gct gta	1728
	Tyr Cys Val Gly Asp Ser Cys Phe Pro Gly Gln Gly Val Ile Ala Val	
	565 570 575	
	gcc ttt tca gga gta atg tgc gct cat cgt gtt gca gct gac tta ggg	1776
	Ala Phe Ser Gly Val Met Cys Ala His Arg Val Ala Ala Asp Leu Gly	
	580 585 590	
25	ttt gaa aaa aaa tca gat gtg ctg gac agt gct ctt ctt aga cta ctt	1824
	Phe Glu Lys Lys Ser Asp Val Leu Asp Ser Ala Leu Leu Arg Leu Leu	
	595 600 605	
30	ggt tgg tta agg aca cta gca tga	1848
	Gly Trp Leu Arg Thr Leu Ala	
	610 615	
35	<210> 122	
	<211> 615	
	<212> PRT	
40	<213> Lycopersicon esculentum	
45	<400> 122	

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 1 5 10 15

5 Cys Lys Thr Val Ala Leu Gly Asp Ser Lys Pro Arg Tyr Asn Lys Gln
 20 25 30

Arg Ser Ser Cys Phe Asp Pro Leu Ile Ile Gly Asn Cys Thr Asp Gln
 10 35 40 45

Gln Gln Leu Cys Gly Leu Ser Trp Gly Val Asp Lys Ala Lys Gly Arg
 50 55 60

15 Arg Gly Gly Thr Val Ser Asn Leu Lys Ala Val Val Asp Val Asp Lys
 65 70 75 80

20 Arg Val Glu Ser Tyr Gly Ser Ser Asp Val Glu Gly Asn Glu Ser Gly
 85 90 95

25 Ser Tyr Asp Ala Ile Val Ile Gly Ser Gly Ile Gly Gly Leu Val Ala
 100 105 110

Ala Thr Gln Leu Ala Val Lys Gly Ala Lys Val Leu Val Leu Glu Lys
 30 115 120 125

Tyr Val Ile Pro Gly Gly Ser Ser Gly Phe Tyr Glu Arg Asp Gly Tyr
 130 135 140

35 Lys Phe Asp Val Gly Ser Ser Val Met Phe Gly Phe Ser Asp Lys Gly
 145 150 155 160

40 Asn Leu Asn Leu Ile Thr Gln Ala Leu Ala Ala Val Gly Arg Lys Leu
 165 170 175

45 Glu Val Ile Pro Asp Pro Thr Thr Val His Phe His Leu Pro Asn Asp

215

	180	185	190
5	Leu Ser Val Arg Ile His Arg Glu Tyr Asp Asp Phe Ile Glu Glu Leu 195 200 205		
10	Val Ser Lys Phe Pro His Glu Lys Glu Gly Ile Ile Lys Phe Tyr Ser 210 215 220		
15	Glu Cys Trp Lys Ile Phe Asn Ser Leu Asn Ser Leu Glu Leu Lys Ser 225 230 235 240		
20	Leu Glu Glu Pro Ile Tyr Leu Phe Gly Gln Phe Phe Lys Lys Pro Leu 245 250 255		
25	Glu Cys Leu Thr Leu Ala Tyr Tyr Leu Pro Gln Asn Ala Gly Ser Ile 260 265 270		
30	Ala Arg Lys Tyr Ile Arg Asp Pro Gly Leu Leu Ser Phe Ile Asp Ala 275 280 285		
35	Glu Cys Phe Ile Val Ser Thr Val Asn Ala Leu Gln Thr Pro Met Ile 290 295 300		
40	Asn Ala Ser Met Val Leu Cys Asp Arg His Phe Gly Gly Ile Asn Tyr 305 310 315 320		
45	Pro Val Gly Gly Val Gly Glu Ile Ala Lys Ser Leu Ala Lys Gly Leu 325 330 335		
50	Asp Asp His Gly Ser Gln Ile Leu Tyr Arg Ala Asn Val Thr Ser Ile 340 345 350		
55	Ile Leu Asp Asn Gly Lys Ala Val Gly Val Lys Leu Ser Asp Gly Arg 355 360 365		

Lys Phe Tyr Ala Lys Thr Ile Val Ser Asn Ala Thr Arg Trp Asp Thr
 370 375 380
 5

Phe Gly Lys Leu Leu Lys Ala Glu Asn Leu Pro Lys Glu Glu Glu Asn
 385 390 395 400

10

Phe Gln Lys Ala Tyr Val Lys Ala Pro Ser Phe Leu Ser Ile His Met
 405 410 415

15

Gly Val Lys Ala Asp Val Leu Pro Pro Asp Thr Asp Cys His His Phe
 420 425 430

20

Val Leu Glu Asp Asp Trp Thr Asn Leu Glu Lys Pro Tyr Gly Ser Ile
 435 440 445

Phe Leu Ser Ile Pro Thr Val Leu Asp Ser Ser Leu Ala Pro Glu Gly
 450 455 460
 25

His His Ile Leu His Ile Phe Thr Thr Ser Ser Ile Glu Asp Trp Glu
 465 470 475 480

30

Gly Leu Ser Pro Lys Asp Tyr Glu Ala Lys Lys Glu Val Val Ala Glu
 485 490 495

35

Arg Ile Ile Ser Arg Leu Glu Lys Thr Leu Phe Pro Gly Leu Lys Ser
 500 505 510

40

Ser Ile Leu Phe Lys Glu Val Gly Thr Pro Lys Thr His Arg Arg Tyr
 515 520 525

45

Leu Ala Arg Asp Ser Gly Thr Tyr Gly Pro Met Pro Arg Gly Thr Pro
 530 535 540

Lys Gly Leu Leu Gly Met Pro Phe Asn Thr Thr Ala Ile Asp Gly Leu
 545 550 555 560

5 Tyr Cys Val Gly Asp Ser Cys Phe Pro Gly Gln Gly Val Ile Ala Val
 565 570 575

10 Ala Phe Ser Gly Val Met Cys Ala His Arg Val Ala Ala Asp Leu Gly
 580 585 590

15 Phe Glu Lys Lys Ser Asp Val Leu Asp Ser Ala Leu Leu Arg Leu Leu
 595 600 605

20 Gly Trp Leu Arg Thr Leu Ala
 610 615

<210> 123

<211> 1233

25 <212> DNA

<213> Tagetes erecta

30

<220>

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35 <222> (1) .. (1233)

<223>

40

<400> 123

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 Met Ala Thr His Lys Leu Leu Gln Phe Thr Thr Asn Leu Pro Pro Ser

45 1 5 10 15 48

	tct tct tca atc tct act ggc tgt tca ctc tcc ccc ttc ttc ctc aaa	96
	Ser Ser Ser Ile Ser Thr Gly Cys Ser Leu Ser Pro Phe Phe Leu Lys	
	20 25 30	
5	tca tct tct cat tcc cct aac cct cgc cga cac cgc cgc tcc gcc gta	144
	Ser Ser Ser His Ser Pro Asn Pro Arg Arg His Arg Arg Ser Ala Val	
	35 40 45	
10	tgc tgc tct ttc gcc tca ctc gac tct gca aaa atc aaa gtc gtt ggc	192
	Cys Cys Ser Phe Ala Ser Leu Asp Ser Ala Lys Ile Lys Val Val Gly	
	50 55 60	
15	gtc ggt ggt ggt ggc aac aat gcc gtt aac cgc atg att ggt agc ggc	240
	Val Gly Gly Gly Gly Asn Asn Ala Val Asn Arg Met Ile Gly Ser Gly	
	65 70 75 80	
20	tta cag ggt gtt gat ttt tac gcc att aac acg gac tca caa gcg ctt	288
	Leu Gln Gly Val Asp Phe Tyr Ala Ile Asn Thr Asp Ser Gln Ala Leu	
	85 90 95	
25	ctg caa tct gtt gca cat aac cct att caa att ggg gag ctt ttg act	336
	Leu Gln Ser Val Ala His Asn Pro Ile Gln Ile Gly Glu Leu Leu Thr	
	100 105 110	
30	cgt gga tta ggt act ggt ggg aac ccg ctt ttg gga gaa cag gct gcg	384
	Arg Gly Leu Gly Thr Gly Gly Asn Pro Leu Leu Gly Glu Gln Ala Ala	
	115 120 125	
35	gag gag tcg aag gaa gcg att ggg aat gcg ctt aaa ggg tcg gat ctt	432
	Glu Glu Ser Lys Glu Ala Ile Gly Asn Ala Leu Lys Gly Ser Asp Leu	
	130 135 140	
40	gtg ttt ata aca gca ggt atg ggt ggt ggg acg ggt tcg ggt gct gct	480
	Val Phe Ile Thr Ala Gly Met Gly Gly Gly Thr Gly Ser Gly Ala Ala	
	145 150 155 160	
45	cca gtt gta gcg cag ata gcg aaa gaa gca ggg tat tta act gtt ggt	528
	Pro Val Val Ala Gln Ile Ala Lys Glu Ala Gly Tyr Leu Thr Val Gly	
	165 170 175	
50	gtt gta acg tac cca ttc agc ttt gaa ggc cgt aaa aga tca gta cag	576
	Val Val Thr Tyr Pro Phe Ser Phe Glu Gly Arg Lys Arg Ser Val Gln	
	180 185 190	

219

	gcg tta gag gct att gag aag ctg caa aag aac gtt gac aca ctt ata	624
	Ala Leu, Glu Ala Ile Glu Lys Leu Gln Lys Asn Val Asp Thr Leu Ile	
	195 200 205	
5	gtg att cca aat gac cgt ttg ctg gat att gct gat gaa aac acg cct	672
	Val Ile Pro Asn Asp Arg Leu Leu Asp Ile Ala Asp Glu Asn Thr Pro	
	210 215 220	
10	ctt cag gat gct ttt ctt ctt gct gat gat gta ctc cgc caa gga gtt	720
	Leu Gln Asp Ala Phe Leu Leu Ala Asp Asp Val Leu Arg Gln Gly Val	
	225 230 235 240	
15	caa gga atc tca gat ata att aca ata cct ggg ctg gta aat gtg gac	768
	Gln Gly Ile Ser Asp Ile Ile Thr Ile Pro Gly Leu Val Asn Val Asp	
	245 250 255	
20	ttt gca gac gtt aaa gca gtc atg aaa gat tct gga act gca atg ctt	816
	Phe Ala Asp Val Lys Ala Val Met Lys Asp Ser Gly Thr Ala Met Leu	
	260 265 270	
	ggg gtc ggt gtt tcc tca agt aaa aac cga gct gaa gaa gca gct gaa	864
	Gly Val Gly Val Ser Ser Ser Lys Asn Arg Ala Glu Glu Ala Ala Glu	
	275 280 285	
25	caa gca act ctt gct cct ttg att gga tca tca att caa tct gct aca	912
	Gln Ala Thr Leu Ala Pro Leu Ile Gly Ser Ser Ile Gln Ser Ala Thr	
	290 295 300	
30	ggg gtt gtt tat aat att acc gga ggg aag gac ata act cta caa gaa	960
	Gly Val Val Tyr Asn Ile Thr Gly Gly Lys Asp Ile Thr Leu Gln Glu	
	305 310 315 320	
35	gtc aac agg gtt tct cag gtg gta aca agt ttg gca gat cca tca gca	1008
	Val Asn Arg Val Ser Gln Val Val Thr Ser Leu Ala Asp Pro Ser Ala	
	325 330 335	
40	aac att ata ttc ggg gca gtg gta gat gag aga tac aac ggg gag att	1056
	Asn Ile Ile Phe Gly Ala Val Val Asp Glu Arg Tyr Asn Gly Glu Ile	
	340 345 350	
	cat gtg acc att gtt gct act ggc ttt gcc cag tcg ttt cag aaa tct	1104
	His Val Thr Ile Val Ala Thr Gly Phe Ala Gln Ser Phe Gln Lys Ser	
	355 360 365	
45	ctt ctt gct gac ccg aaa gga gca aaa ctt gtt gat aga aat caa gaa	1152

220

Leu Leu Ala Asp Pro Lys Gly Ala Lys Leu Val Asp Arg Asn Gln Glu
 370 375 380

5 cct aca caa cct ttg act tcc gcg aga tct ttg aca aca cct tct cct 1200
 Pro Thr Gln Pro Leu Thr Ser Ala Arg Ser Leu Thr Thr Pro Ser Pro
 385 390 395 400

10 gct ccg tct cgg tct agg aaa ctc ttc ttt taa 1233
 Ala Pro Ser Arg Ser Arg Lys Leu Phe Phe
 405 410

<210> 124

15 <211> 410

<212> PRT

20 <213> Tagetes erecta

<400> 124

25 Met Ala Thr His Lys Leu Leu Gln Phe Thr Thr Asn Leu Pro Pro Ser
 1 5 10 15

30 Ser Ser Ser Ile Ser Thr Gly Cys Ser Leu Ser Pro Phe Phe Leu Lys
 20 25 30

35 Ser Ser Ser His Ser Pro Asn Pro Arg Arg His Arg Arg Ser Ala Val
 35 40 45

40 Cys Cys Ser Phe Ala Ser Leu Asp Ser Ala Lys Ile Lys Val Val Gly
 50 55 60

Val Gly Gly Gly Gly Asn Asn Ala Val Asn Arg Met Ile Gly Ser Gly
 65 70 75 80

45 Leu Gln Gly Val Asp Phe Tyr Ala Ile Asn Thr Asp Ser Gln Ala Leu

5	Leu	Gln	Ser	Val	Ala	His	Asn	Pro	Ile	Gln	Ile	Gly	Glu	Leu	Leu	Thr	100	105	110
10	Arg	Gly	Leu	Gly	Thr	Gly	Gly	Asn	Pro	Leu	Leu	Gly	Glu	Gln	Ala	Ala	115	120	125
15	Glu	Glu	Ser	Lys	Glu	Ala	Ile	Gly	Asn	Ala	Leu	Lys	Gly	Ser	Asp	Leu	130	135	140
20	Val	Phe	Ile	Thr	Ala	Gly	Met	Gly	Gly	Gly	Thr	Gly	Ser	Gly	Ala	Ala	145	150	155
25	Pro	Val	Val	Ala	Gln	Ile	Ala	Lys	Glu	Ala	Gly	Tyr	Leu	Thr	Val	Gly	165	170	175
30	Val	Val	Thr	Tyr	Pro	Phe	Ser	Phe	Glu	Gly	Arg	Lys	Arg	Ser	Val	Gln	180	185	190
35	Ala	Leu	Glu	Ala	Ile	Glu	Lys	Leu	Gln	Lys	Asn	Val	Asp	Thr	Leu	Ile	195	200	205
40	Val	Ile	Pro	Asn	Asp	Arg	Leu	Leu	Asp	Ile	Ala	Asp	Glu	Asn	Thr	Pro	210	215	220
45	Leu	Gln	Asp	Ala	Phe	Leu	Leu	Ala	Asp	Asp	Val	Leu	Arg	Gln	Gly	Val	225	230	235
50	Gln	Gly	Ile	Ser	Asp	Ile	Ile	Thr	Ile	Pro	Gly	Leu	Val	Asn	Val	Asp	245	250	255
55	Phe	Ala	Asp	Val	Lys	Ala	Val	Met	Lys	Asp	Ser	Gly	Thr	Ala	Met	Leu	260	265	270

Gly Val Gly Val Ser Ser Ser Lys Asn Arg Ala Glu Glu Ala Ala Glu
 275 280 285
 5

Gln Ala Thr Leu Ala Pro Leu Ile Gly Ser Ser Ile Gln Ser Ala Thr
 290 295 300

10

Gly Val Val Tyr Asn Ile Thr Gly Gly Lys Asp Ile Thr Leu Gln Glu
 305 310 315 320

15

Val Asn Arg Val Ser Gln Val Val Thr Ser Leu Ala Asp Pro Ser Ala
 325 330 335

20

Asn Ile Ile Phe Gly Ala Val Val Asp Glu Arg Tyr Asn Gly Glu Ile
 340 345 350

25

His Val Thr Ile Val Ala Thr Gly Phe Ala Gln Ser Phe Gln Lys Ser
 355 360 365

30

Leu Leu Ala Asp Pro Lys Gly Ala Lys Leu Val Asp Arg Asn Gln Glu
 370 375 380

35

Pro Thr Gln Pro Leu Thr Ser Ala Arg Ser Leu Thr Thr Pro Ser Pro
 385 390 395 400

40

Ala Pro Ser Arg Ser Arg Lys Leu Phe Phe
 405 410

<210> 125
 <211> 891
 <212> DNA

<213> Tagetes erecta

5 <220>

<221> CDS

<222> (1)..(891)

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<223>

15 <400> 125

atg aca tcc ctg agg ttt cta aca gaa ccc tca ctt gta tgc tca tcc 48
 Met Thr Ser Leu Arg Phe Leu Thr Glu Pro Ser Leu Val Cys Ser Ser
 1 5 10 15

20 act ttc ccc aca ttc aat ccc cta cac aaa acc cta act aaa cca aca 96
 Thr Phe Pro Thr Phe Asn Pro Leu His Lys Thr Leu Thr Lys Pro Thr
 20 25 30

25 cca aaa ccc tac cca aag cca cca cca att cgc tcc gtc ctt caa tac 144
 Pro Lys Pro Tyr Pro Lys Pro Pro Pro Ile Arg Ser Val Leu Gln Tyr
 35 40 45

30 aat cgc aaa cca gag ctc gcc gga gac act cca cga gtc gtc gca atc 192
 Asn Arg Lys Pro Glu Leu Ala Gly Asp Thr Pro Arg Val Val Ala Ile
 50 55 60

35 gac gcc gac gtt ggt cta cgt aac ctc gat ctt ctt ctc ggt ctc gaa 240
 Asp Ala Asp Val Gly Leu Arg Asn Leu Asp Leu Leu Leu Gly Leu Glu
 65 70 75 80

aac cgc gtc aat tac acc gtc gtt gaa gtt ctc aac ggc gat tgc aga 288
 Asn Arg Val Asn Tyr Thr Val Val Glu Val Leu Asn Gly Asp Cys Arg
 85 90 95

40 ctc gac caa gcc cta gtt cgt gat aaa cgc tgg tca aat ttc gaa ttg 336
 Leu Asp Gln Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu
 100 105 110

45 ctt tgt att tca aaa cct agg tca aaa ttg cct tta gga ttt ggg gga 384
 Leu Cys Ile Ser Lys Pro Arg Ser Lys Leu Pro Leu Gly Phe Gly Gly

224

	115	120	125	
	aaa gct tta gtt tgg ctt gat gca tta aaa gat agg caa gaa ggt tgc			432
	Lys Ala Leu Val Trp Leu Asp Ala Leu Lys Asp Arg Gln Glu Gly Cys			
5	130	135	140	
	ccg gat ttt ata ctt ata gat tgt cct gca ggt att gat gcc ggg ttc			480
	Pro Asp Phe Ile Leu Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe			
	145	150	155	160
10				
	ata acc gcc att aca ccg gct aac gaa gcc gta tta gtt aca aca cct			528
	Ile Thr Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro			
	165	170	175	
15				
	gat att act gca ttg aga gat gca gat aga gtt aca ggc ttg ctt gaa			576
	Asp Ile Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu			
	180	185	190	
20				
	tgt gat gga att agg gat att aaa atg att gtg aac aga gtt aga act			624
	Cys Asp Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr			
	195	200	205	
25				
	gat ttg ata agg ggt gaa gat atg atg tca gtt ctt gat gtt caa gag			672
	Asp Leu Ile Arg Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu			
	210	215	220	
30				
	atg ttg gga ttg tca ttg ttg agt gat acc cga gga ttc gaa gtg att			720
	Met Leu Gly Leu Ser Leu Leu Ser Asp Thr Arg Gly Phe Glu Val Ile			
	225	230	235	240
35				
	cgg agt acg aat aga ggg ttt ccg ctt gtg ttg aac aag cct ccg act			768
	Arg Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr			
	245	250	255	
40				
	tta gca gga ttg gca ttt gag cag gct gct tgg aga ttg gtt gag caa			816
	Leu Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln			
	260	265	270	
45				
	gat agc atg aag gct gtg atg gtg gag gaa gaa cct aaa aag agg gga			864
	Asp Ser Met Lys Ala Val Met Val Glu Glu Glu Pro Lys Lys Arg Gly			
	275	280	285	
	ttt ttc tcg ttt ttt gga ggt tag tga			891
	Phe Phe Ser Phe Phe Gly Gly			
	290	295		

<210> 126

5 <211> 295

<212> PRT

10 <213> Tagetes erecta

<400> 126

15 Met Thr Ser Leu Arg Phe Leu Thr Glu Pro Ser Leu Val Cys Ser Ser
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20 25 30

25 Pro Lys Pro Tyr Pro Lys Pro Pro Pro Ile Arg Ser Val Leu Gln Tyr
35 40 45

30 Asn Arg Lys Pro Glu Leu Ala Gly Asp Thr Pro Arg Val Val Ala Ile
50 55 60

Asp Ala Asp Val Gly Leu Arg Asn Leu Asp Leu Leu Gly Leu Glu
65 70 75 80

35 Asn Arg Val Asn Tyr Thr Val Val Glu Val Leu Asn Gly Asp Cys Arg
85 90 95

40 Leu Asp Gln Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu
100 105 110

45 Leu Cys Ile Ser Lys Pro Arg Ser Lys Leu Pro Leu Gly Phe Gly Gly
115 120 125

Lys Ala Leu Val Trp Leu Asp Ala Leu Lys Asp Arg Gln Glu Gly Cys
130 135 140

5

Pro Asp Phe Ile Leu Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe
145 150 155 160

10

Ile Thr Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro
165 170 175

15

Asp Ile Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu
180 185 190

20

Cys Asp Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr
195 200 205

Asp Leu Ile Arg Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu
210 215 220

25

Met Leu Gly Leu Ser Leu Leu Ser Asp Thr Arg Gly Phe Glu Val Ile
225 230 235 240

30

Arg Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr
245 250 255

35

Leu Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln
260 265 270

40

Asp Ser Met Lys Ala Val Met Val Glu Glu Glu Pro Lys Lys Arg Gly
275 280 285

Phe Phe Ser Phe Phe Gly Gly
290 295

45

<210> 127

<211> 332

5 <212> DNA

<213> Tagetes erecta

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<220>

<221> CDS

15 <222> (1)..(330)

<223>

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<400> 127

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 Lys Leu Ala Arg Ala Ser Leu Tyr Phe Tyr Thr Ser Met Ala Ala Ala
 1 5 10 15

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att gct gtc cct tgt agc tca aga cca ttt ggc tta ggt cga atg cgg 96
 Ile Ala Val Pro Cys Ser Ser Arg Pro Phe Gly Leu Gly Arg Met Arg
 20 25 30

30

tta ctt ggt cat aaa ccc aca acc ata act tgt cac ttc ccc ttt tct 144
 Leu Leu Gly His Lys Pro Thr Thr Ile Thr Cys His Phe Pro Phe Ser
 35 40 45

35

ttt tct atc aaa tca ttt acc cca att gtt agg ggc aga aga tgt act 192
 Phe Ser Ile Lys Ser Phe Thr Pro Ile Val Arg Gly Arg Arg Cys Thr
 50 55 60

40

gtt tgt ttt gtt gcc ggt ggc gac agt aat agt aac agt aat aat aat 240
 Val Cys Phe Val Ala Gly Gly Asp Ser Asn Ser Asn Ser Asn Asn Asn
 65 70 75 80

agt gac agt aat agt aat aat ccg ggt ctg gat tta aac ccg gcg gtt 288
 Ser Asp Ser Asn Ser Asn Asn Pro Gly Leu Asp Leu Asn Pro Ala Val
 85 90 95

45

228

atg aac cgt aac cgt ttg gtt gaa gaa aaa atg gag agg tcg ac 332
 Met Asn Arg Asn Arg Leu Val Glu Glu Lys Met Glu Arg Ser
 100 105 110

5

<210> 128

<211> 110

10

<212> PRT

<213> Tagetes erecta

15

<400> 128

Lys Leu Ala Arg Ala Ser Leu Tyr Phe Tyr Thr Ser Met Ala Ala Ala
 1 5 10 15

20

Ile Ala Val Pro Cys Ser Ser Arg Pro Phe Gly Leu Gly Arg Met Arg
 20 25 30

25

Leu Leu Gly His Lys Pro Thr Thr Ile Thr Cys His Phe Pro Phe Ser
 35 40 45

30

Phe Ser Ile Lys Ser Phe Thr Pro Ile Val Arg Gly Arg Arg Cys Thr
 50 55 60

35

Val Cys Phe Val Ala Gly Gly Asp Ser Asn Ser Asn Ser Asn Asn Asn
 65 70 75 80

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Ser Asp Ser Asn Ser Asn Asn Pro Gly Leu Asp Leu Asn Pro Ala Val
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Met Asn Arg Asn Arg Leu Val Glu Glu Lys Met Glu Arg Ser
 100 105 110

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30 gca aaa ctg act cca gta ctg aga agt aaa tct cag ttt aag ggg ctt 97
 Ala Lys Leu Thr Pro Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu
 20 25 30

35 ttc att gct att gtc att gtt agc gca tgg gtc att agc ctg agt tta 145
 Phe Ile Ala Ile Val Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu
 35 40 45

40 tta ctt tcc ctt gac atc tca aag cta aaa ttt tgg atg tta ttg cct 193
 Leu Leu Ser Leu Asp Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro
 50 55 60

gtt ata cta tgg caa aca ttt tta tat acg gga tta ttt att aca tct 241
 Val Ile Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser
 65 70 75

45 cat gat gcc atg cat ggc gta gta ttt ccc caa aac acc aag att aat 289

231

	His Asp Ala Met His Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn	
	80 85 90 95	
5	cat ttg att gga aca ttg acc cta tcc ctt tat ggt ctt tta cca tat His Leu Ile Gly Thr Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr 100 105 110	337
10	caa aaa cta ttg aaa aaa cat tgg tta cac cac cac aat cca gca agc Gln Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser 115 120 125	385
15	tca ata gac ccg gat ttt cac aat ggt aaa cac caa agt ttc ttt gct Ser Ile Asp Pro Asp Phe His Asn Gly Lys His Gln Ser Phe Phe Ala 130 135 140	433
20	tgg tat ttt cat ttt atg aaa ggt tac tgg agt tgg ggg caa ata att Trp Tyr Phe His Phe Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile 145 150 155	481
25	gcg ttg act att att tat aac ttt gct aaa tac ata ctc cat atc cca Ala Leu Thr Ile Ile Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro 160 165 170 175	529
30	agt gat aat cta act tac ttt tgg gtg cta ccc tcg ctt tta agt tca Ser Asp Asn Leu Thr Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser 180 185 190	577
35	tta caa tta ttc tat ttt ggt act ttt tta ccc cat agt gaa cca ata Leu Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile 195 200 205	625
40	ggg ggt tat gtt cag cct cat tgt gcc caa aca att agc cgt cct att Gly Gly Tyr Val Gln Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile 210 215 220	673
45	tgg tgg tca ttt atc acg tgc tat cat ttt ggc tac cac gag gaa cat Trp Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Glu Glu His 225 230 235	721
50	cac gaa tat cct cat att tct tgg tgg cag tta cca gaa att tac aaa His Glu Tyr Pro His Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys 240 245 250 255	769
55	gca aaa tagtctagag catgcgc Ala Lys	792

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 20 Lys Leu Thr Pro Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe
 20 25 30
 Ile Ala Ile Val Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu
 25 35 40 45
 Leu Ser Leu Asp Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val
 50 55 60
 30 Ile Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His
 65 70 75 80
 35 Asp Ala Met His Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His
 85 90 95
 40 Leu Ile Gly Thr Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln
 100 105 110
 45 Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser Ser
 115 120 125

Ile Asp Pro Asp Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp
 130 135 140
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Tyr Phe His Phe Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala
 145 150 155 160

10

Leu Thr Ile Ile Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser
 165 170 175

15

Asp Asn Leu Thr Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu
 180 185 190

20

Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly
 195 200 205

25

Gly Tyr Val Gln Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp
 210 215 220

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Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His
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Lys

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tcggttcatt ctaatgaata tatcaccctg tactatcgta tttttatgaa taatattctc 180

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cggttcaattt actgattgtc caagctcgag 210

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aagcttggtt gatcagaaga agaagaagaa gatgaact

38

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<210> 138

<211> 652

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<213> Arabidopsis thaliana

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cccgggaatt cttcattatt tcgattttga tttcgtgacc agcgaacgca gaataccttg 60

10 ttgtgtaata ctttaccgt gtaaatcaaa aacaaaaagg cttttgagct tttttagtt 120

gaatttctct ggctgatctt tctgtacag attcatatat ctgcagagac gatatcattg 180

attatttgag ctctctttga actatttcgt gtaatttggg atgagagctc tatgtatgtg 240

15 tgtaaacttt gaagacaaca agaaaggtaa caagtgaggg agggatgact ccatgtcaaa 300

atagatgtca taagaggcgc atcaataagt gcttgagccc attagctagc ccagtaacta 360

20 ccagattgtg agatggatgt gtgaacagtt ttttttttga tgtaggactg aaatgtgaac 420

aacaggcgca tgaaaaggcta aattaggaca atgataagca gaaataactt atcctctcta 480

acacttggcc tcacattgcc cttcacacaa tccacacaca tccaatcaca acctcatcat 540

25 atatctcccg ctaatctttt tttctttgat cttttttttt ttgcttatta tttttttgac 600

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gagctctagc gcaatcttat gtggtacaa

29

10

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catttggtta ctctctgctg tggtagttgg catatccaca ttgtctcctt ccacttttat 180

gacaattacg tgaaagttat ggggtgtttt gtctattttt gtcgaggcct ttcttttcct 240

20

tccaggttgt tgaagatggt ccaattcgat tagaataatg ttttgagctt tagcatattc 300

tctctcgttt acacgattat agtaataatg atataggatg acagaagttg acacataaat 360

tttttattct ctccatttac tttaatccaa atctcaccta ccctaaactt ctttaatatg 420

25

tattcaatag tctatccgag taaattgtaa atttaacaac cattgataat attgacacct 480

actaacatat actagtaaag agaataattaa catggcacat ataatttgat gcaaaatgag 540

30

tatgatgaaa tttaaacccta aaatctcttg attttgacag tgtcaccttg acttggttaac 600

taataagtca tgtttttagtg gcagaaagac aaactcatcc accaactgta tagcaataaa 660

aaatagaaga atcttcctga ggcaaagttt tggaaaaatt aagagtggct gagatttaat 720

35

ttcaacagga attagttcca cttaactttt aggttacgat acagtgctaa ttaaataact 780

taattgtatt agatatttct tgcacctaaa aaatttaaaa actgaaaaaa ggtagcaatc 840

40

aaaataaaca aaaggacaaa ataagtgaag ggtacagcca ccaaccctgg cggctcactg 900

tttgttggtt aaaacgtaga cttacaccta ccaaaatcta caactaaaat gaggaataa 960

tactttgccc aaaattacca agaaaagaaa aagaaaggaa tcccttaata ttactctcct 1020

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ccatttcaca ataaatatcc tagtttgact taaatttagag tttaaaaaat gaaagacgac 1080
 ttttaaaact tgtaatctaa aataaatcat agttaaatgt gtggctataa atcattgtat 1140
 5 taacggtaaa gtggtaagtt taaaagttaa ttgttttcaa atataaaatt gtactatcat 1200
 tctttttgga atggactaat aagaaaacta tgacatccat tatggagcgg agggagtatc 1260
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 20 gtagttggtg aagctaagtca gcgaatcca ttacctcca ctctaccta ccccttcac 1680
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	ggt gca ata gag caa tta agt gct aaa gaa gat act gtt tgg ggg ctg	97
	Val Ala Ile Glu Gln Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu	
	20 25 30	
15	gtg att gtc ata gta att att agt ctt tgg gta gct agt ttg gct ttt	145
	Val Ile Val Ile Val Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe	
	35 40 45	
20	tta cta gct att aat tat gcc aaa gtc cca att tgg ttg ata cct att	193
	Leu Leu Ala Ile Asn Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile	
	50 55 60	
	gca ata gtt tgg caa atg ttc ctt tat aca ggg cta ttt att act gca	241
25	Ala Ile Val Trp Gln Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala	
	65 70 75	
	cat gat gct atg cat ggg tca gtt tat cgt aaa aat ccc aaa att aat	289
	His Asp Ala Met His Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn	
30	80 85 90 95	
	aat ttt atc ggt tca cta gct gta gcg ctt tac gct gtg ttt cca tat	337
	Asn Phe Ile Gly Ser Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr	
	100 105 110	
35	caa cag atg tta aag aat cat tgc tta cat cat cgt cat cct gct agc	385
	Gln Gln Met Leu Lys Asn His Cys Leu His His Arg His Pro Ala Ser	
	115 120 125	
40	gaa gtt gac cca gat ttt cat gat ggt aag aga aca aac gct att ttc	433
	Glu Val Asp Pro Asp Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe	
	130 135 140	
	tgg tat ctc cat ttc atg ata gaa tac tcc agt tgg caa cag tta ata	481
45	Trp Tyr Leu His Phe Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile	

243

	145	150	155	
	gta cta act atc cta ttt aat tta gct aaa tac gtt ttg cac atc cat			529
	Val Leu Thr Ile Leu Phe Asn Leu Ala Lys Tyr Val Leu His Ile His			
5	160	165	170	175
	caa ata aat ctc atc tta ttt tgg agt att cct cca att tta agt tcc			577
	Gln Ile Asn Leu Ile Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser			
		180	185	190
10				
	att caa ctg ttt tat ttc gga aca ttt ttg cct cat cga gaa ccc aag			625
	Ile Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys			
		195	200	205
15				
	aaa gga tat gtt tat ccc cat tgc agc caa aca ata aaa ttg cca act			673
	Lys Gly Tyr Val Tyr Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr			
		210	215	220
	ttt ttg tca ttt atc gct tgc tac cac ttt ggt tat cat gaa gaa cat			721
20	Phe Leu Ser Phe Ile Ala Cys Tyr His Phe Gly Tyr His Glu Glu His			
		225	230	235
	cat gag tat ccc cat gta cct tgg tgg caa ctt cca tct gta tat aag			769
	His Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys			
25	240	245	250	255
	cag aga gta ttc aac aat tca gta acc aat tcg taatctagag catgcgc			819
	Gln Arg Val Phe Asn Asn Ser Val Thr Asn Ser			
		260	265	
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Ala Ile Glu Gln Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val
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 5

Ile Val Ile Val Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu
 35 40 45

10

Leu Ala Ile Asn Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala
 50 55 60

15

Ile Val Trp Gln Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
 65 70 75 80

20

Asp Ala Met His Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn
 85 90 95

Phe Ile Gly Ser Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln
 100 105 110

25

Gln Met Leu Lys Asn His Cys Leu His His Arg His Pro Ala Ser Glu
 115 120 125

30

Val Asp Pro Asp Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp
 130 135 140

35

Tyr Leu His Phe Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val
 145 150 155 160

40

Leu Thr Ile Leu Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln
 165 170 175

Ile Asn Leu Ile Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile
 180 185 190

45

245

Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys
195 200 205

5

Gly Tyr Val Tyr Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe
210 215 220

10

Leu Ser Phe Ile Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His
225 230 235 240

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Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln
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Arg Val Phe Asn Asn Ser Val Thr Asn Ser
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247

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	1 5 10 15	
5	agc cta ggt ttg tta ctt tat att gat ata tcc caa ttc aag ttt tgg	97
	Ser Leu Gly Leu Leu Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp	
	20 25 30	
	atg ttg tta ccg ctc ata ttt tgg caa aca ttt tta tat acg gga tta	145
10	Met Leu Leu Pro Leu Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu	
	35 40 45	
	ttt att aca gct cat gat gcc atg cat ggg gta gtt ttt ccc aaa aat	193
	Phe Ile Thr Ala His Asp Ala Met His Gly Val Val Phe Pro Lys Asn	
15	50 55 60	
	ccc aaa atc aac cat ttc att ggc tca ttg tgc ctg ttt ctt tat ggt	241
	Pro Lys Ile Asn His Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly	
	65 70 75	
20	ctt tta cct tat caa aaa ctt tta aaa aag cat tgg cta cat cac cat	289
	Leu Leu Pro Tyr Gln Lys Leu Leu Lys Lys His Trp Leu His His His	
	80 85 90 95	
25	aat cca gcc agt gaa aca gat cca gat ttt cac aac ggg aag cag aaa	337
	Asn Pro Ala Ser Glu Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys	
	100 105 110	
	aac ttt ttt gct tgg tat tta tat ttt atg aag cgt tac tgg agt tgg	385
30	Asn Phe Phe Ala Trp Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp	
	115 120 125	
	tta caa att atc aca tta atg att att tat aac tta cta aaa tat ata	433
	Leu Gln Ile Ile Thr Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile	
35	130 135 140	
	tgg cat ttt cca gag gat aat atg act tat ttt tgg gta gtt ccc tca	481
	Trp His Phe Pro Glu Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser	
	145 150 155	
40	att tta agt tct tta caa tta ttt tat ttt gga act ttt cta ccc cac	529
	Ile Leu Ser Ser Leu Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His	
	160 165 170 175	
45	agt gag cct gta gaa ggt tat aaa gag cct cat cgt tcc caa act att	577

Ser Glu Pro Val Glu Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile
 180 185 190

5 agc cgt ccc att tgg tgg tca ttt ata act tgt tac cat ttt ggt tat 625
 Ser Arg Pro Ile Trp Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr
 195 200 205

10 cat tac gaa cat cat gaa tac ccc cat gtt cct tgg tgg caa tta cca 673
 His Tyr Glu His His Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro
 210 215 220

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35 Leu Gly Leu Leu Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp Met
 20 25 30

Leu Leu Pro Leu Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe
 35 40 45

40 Ile Thr Ala His Asp Ala Met His Gly Val Val Phe Pro Lys Asn Pro
 50 55 60

45 Lys Ile Asn His Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly Leu

65

70

75

80

Leu Pro Tyr Gln Lys Leu Leu Lys Lys His Trp Leu His His His Asn
 5 85 90 95

Pro Ala Ser Glu Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys Asn
 10 100 105 110

Phe Phe Ala Trp Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp Leu
 115 120 125
 15

Gln Ile Ile Thr Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile Trp
 130 135 140

His Phe Pro Glu Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser Ile
 145 150 155 160
 20

Leu Ser Ser Leu Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser
 165 170 175
 25

Glu Pro Val Glu Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile Ser
 180 185 190
 30

Arg Pro Ile Trp Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His
 195 200 205
 35

Tyr Glu His His Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Glu
 210 215 220
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Ile Tyr Lys Met Ser Lys Ser Asn Leu
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<220>

35 <221> Primer

<222> (1)..(25)

<223>

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<400> 151

45 ctcgagctta cgagcatttt ctaag

25

<210> 152

<211> 25

<212> DNA

<213> Artificial sequence

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<221> Primer

<222> (1)..(25)

<223>

<400> 152

gaattcccaa taataatcta cagcc

25

<210> 153

<211> 25

<212> DNA

<213> Artificial sequence

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<223>

<400> 153
aagcttgac gagcctctct ctatt

25

5 <210> 154

<211> 25

<212> DNA

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<213> Artificial sequence

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<222> (1)..(25)

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<223>

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gtcgacctct ccattttttc ttcaa

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<210> 155

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<211> 22

<212> DNA

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5 <400> 155
gaattcggca cgagcctctc tc

22

<210> 156

10 <211> 23

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15 <213> Artificial sequence

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20 <221> Primer

<222> (1)..(23)

<223>

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<400> 156
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23

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<210> 157

<211> 24

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<212> DNA

<213> Artificial sequence

40

<220>

<221> Primer

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<222> (1)..(24)

<223>

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<400> 157

gagctctagc gcaatcttat gtgg

24

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<210> 158

<211> 22

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<212> DNA

<213> Artificial sequence

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<221> Primer

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<222> (1)..(22)

<223>

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<400> 158

ccatggttct cacttctgta tg

22

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<210> 159

<211> 25

<212> DNA

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<213> Artificial sequence

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<221> Primer

5 <222> (1)..(25)

<223>

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<400> 159

aagcttgcacat ggcggccgga atttc

25

15 <210> 160

<211> 307

<212> DNA

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<213> Vicia faba

25 <220>

<221> Terminator

<222> (1)..(307)

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<223>

35 <400> 160

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atttagaatt gctgtagtca agaacatcag ttctaaaata ttaataaagt tatggccttt 120

40 tgacatatgt gtttcgataa aaaaatcaaa ataaattgag atttattcga aatacaatga 180

aagtttgcag atatgagata tgtttctaca aaataataac ttaaaaactca actatatgct 240

aatgtttttc ttggtgtggt tcatagaaaa ttgtatccgt ttcttagaaa atgctcgtaa 300

45

gctcgag

5

<210> 161

<211> 1020

<212> DNA

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<213> Lycopersicon esculentum

15

<220>

<221> misc_feature

<222> (1)..(1020)

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<223> Nucleic acid encoding a β -hydroxylase

25

<400> 161

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ataaccggtt tctcagtcca aaatccgcct caaccgcccc gccggttctg ttcttctctc 120

cgtaactcg caattttggc gcaattttgc tgtctagaag aaagccgaga ttggcggttt 180

30

gttttgtgct ggagaaatgag aaattgaata gtactatcga aagtgagagt gaagtaatag 240

aggatcggat acaagtagag attaatgagg agaagagttt agctgccagt tggctggcgg 300

35

agaaattggc gaggaagaaa tcggagaggt ttacttatct tgtggcagct gtgatgtcta 360

gtttggggat tacttctatg gcgattttgg cggtttatta cagattttca tggcaaatgg 420

agggtggaga agtgcctttt tctgaaatgt tagctacatt cactctctcg tttggcgctg 480

40

ccgtaggaat ggagtactgg gcgagatggg ctcatagagc actatggcat gcttctttat 540

ggcacatgca cgagtcgcac catagaccaa gagaaggacc ttttgagatg aacgacgttt 600

45

tcgccataac aaatgctgtt ccagctatag gtcttctttc ctacggtttc ttccataaag 660

257

	ggatcgtccc tggcctctgt ttcggcgctg gattggggat cacagtatctt gggatggctt	720
	acatgttcgt tcacgatgga ctggttcata agagatttcc cgtagggcct attgccaaacg	780
5	tgccttactt tcggagggtg gctgcagcac atcagcttca tcactcggac aaatttgatg	840
	gtgtcccata tggcttggtt ctaggacctt aggaattgga agaagtagga ggacttgaag	900
10	agttagaaaa ggaagtcaac cgaaggatta aaatttctaa gggattatta tgatcaaaag	960
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	<211> 1802	
	<212> DNA	
20	<213> Petunia hybrida	
25	<220>	
	<221> Promoter	
	<222> (1)..(1802)	
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40	catttggtta ctctctgctg tggtagttgg catatccaca ttgtctcctt ccacttttat	180
	gacaattacg tgaaagttat ggggtgtttt gtctattttt gtcgaggcct ttcttttcct	240
45	tccaggttgt tgaagatggt ccaattcgat tagaataatg ttttgagctt tagcatattc	300

	tctctcgttt acacgattat agtaataatg atataggatg acagaagttg acacataaat	360
	tttttattct ctccatttac tttaatccaa atctcaccta ccctaaactt ctttaatatg	420
5	tattcaatag tctatccgag taaattgtaa atttaacaac cattgataat attgacacct	480
	actaacatat actagtaaag agaattattaa catggcacat ataatttgat gcaaaatgag	540
10	tatgatgaaa tttaaaccca aaatctcttg attttgacag tgtcaccttg acttggttaac	600
	taataagtca tgttttagtg gcagaaagac aaactaatcc accaactgta tagcaataaa	660
	aaatagaaga atcttcctga ggcaaagttt tggaaaaatt aagagtggct gagatttaat	720
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	aaaataaaca aaaggacaaa ataagtgaag ggtacagcca ccaaccctgg cggctcactg	900
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	tactttgccc aaaattacca agaaaagaaa aagaaaggaa tcccttaata ttactctcct	1020
25	ccatttcaca ataaatatcc tagtttgact taaattagag tttaaaaaat gaaagacgac	1080
	ttttaaaact tgtaatctaa aataaatcat agttaaatgt gtggctataa atcattgtat	1140
	taacggtaaa gtggtaagt taaaagttaa ttgttttcaa atataaaatt gtactatcat	1200
30	tctttttgga atggactaat aagaaaacta tgacatccat tatggagcgg agggagtatc	1260
	tccttttaac aataaccttt gtccttcaa ttcaattatc agtatgcaa cattaaaaat	1320
35	tattattgat gtaaagtacc acatcatcct taatgataga atcatcgtag aacgcttttc	1380
	caggcacaca ttcaaactag ttagaccagt accacacatc gaatattcca gacttctttg	1440
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40	cccaaaataa tatatacgtc ggggtgaaaa ctataaaatg ttgacaaaa atgtcaaatt	1560
	aatatatcaa tctgcaacaa ccttttcacc ttgagaacac agctgaaatt ttttacaag	1620
45	gtagttggtg aagctagtca gcgaatccca ttaccttcca ctctacctaa ccccttcac	1680

caacaacaaa tttctgtaat ttaaaaacta gccaaaaaag aactctcttt tacaaagagc 1740
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5 gg 1802

<210> 163
10 <211> 332
<212> DNA
15 <213> Tagetes erecta

<220>
20 <221> misc_feature
<222> (1)..(332)

25 <223> β -Hydroxylase sense fragment

<400> 163
30 aagcttgac gagcctctct ctatcttttac acttcaatgg cggcagcaat tgctgtccct 60
tgtagctcaa gaccatttgg cttaggtcga atgcggttac ttggtcataa acccacaacc 120
ataacttgct acttcccctt ttctttttct atcaaatcat ttacccaat tgtagggggc 180
35 agaagatgta ctgtttggtt tggtgccggt ggcgacagta atagtaacag taataataat 240
agtgacagta atagtaataa tccgggtctg gatttaaacc cggcggttat gaaccgtaac 300
40 cgtttggttg aagaaaaaat ggagaggtcg ac 332

<210> 164

<211> 332

<212> DNA

5 <213> *Tagetes erecta*

<220>

10

<221> misc_feature

<222> (1)..(332)

15 <223> β -Hydroxylase antisense fragment

<400> 164

20 gaattcggca cgagcctctc tctattttta cacttcaatg gcggcagcaa ttgctgtccc 60

ttgtagctca agaccatttg gcttaggtcg aatgcgggta cttggtcata aaccacaac 120

cataacttgt cacttcccct tttctttttc tatcaaata tttaccccaa ttgttagggg 180

25 cagaagatgt actgtttggt ttgttgccgg tggcgacagt aatagtaaca gtaataataa 240

tagtgacagt aatagtaata atccgggtct ggatttaaac ccggcggtta tgaaccgtaa 300

30 ccgtttggtt gaagaaaaaa tggagaggat cc 332

<210> 165

35 <211> 996

<212> DNA

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<220>

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<222> (1)..(996)

5 <223>

<400> 165

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	ctcaagacca ttgggcttag gtcgaatgcg gttacttggt cataaaccca caaccataac	120
	ttgtcacttc cccttttctt ttctatcaa atcatttacc ccaattgta ggggcagaag	180
15	atgtactgtt tgttttgttg ccggtggcga cagtaatagt aacagtaata ataatagtg	240
	cagtaatagt aataatccgg gtctggattt aaaccggcg gttatgaacc gtaaccgttt	300
20	ggttgaagaa aaaatggaga ggaaaaaatc ggaacgattt acttatcttg ttgcagctat	360
	tatgtctact ttggaatta cttcaatggc ggttatggcg gtttattacc ggttttcatg	420
	gcaaatggag ggtggagaaa ttccttatgt ggagatgttt ggtacatttg ctctctccgt	480
25	tggtgctgcg gtaggaatgg agtattgggc aagatgggct catgaggcac tatggcatgc	540
	ttctttgtgg cacatgcatg agtcacacca taagccacga gaaggtccgt ttgagcttaa	600
30	tgatgtgttt gctataacaa atgcgggtccc ggccattgcg ttgcttagtt atgggttttt	660
	ccacaaaggc ataattccgg gtctttgttt tggggcgga ctgggaatta cgggtgtttg	720
	aatggcgat atgttcgtcc acgacgggct agttcacaga agattccaag tgggtccgat	780
35	tgcaatgtt ccctatcttc gaaggggtgc agcggctcat cagctgcac acacggaaaa	840
	atttaatggg gttccttatg gcttgttctt gggacctaa gagctagaag aagtgggtgg	900
40	tacggaagaa ttggacaagg agattcaaag aagaattaa ttgtataata atactaaata	960
	aataaatttt gtataaaatt aatataattt aatgat	996

<210> 166

<211> 19

5 <212> DNA

<213> Artificial sequence

10

<220>

<221> Primer

15 <222> (1)..(19)

<223>

20

<400> 166

tgccaaagta actctttat

19

25 <210> 167

<211> 19

<212> DNA

30

<213> Artificial sequence

35 <220>

<221> Primer

<222> (1)..(19)

40

<223>

45 <400> 167

aggtgcatga ccaagtaac

19

<210> 168

5

<211> 1033

<212> DNA

10 <213> Arabidopsis thaliana

<220>

15

<221> Promoter

<222> (1)..(1033)

20 <223> P76

<400> 168

25 aggtgcatga ccaagtaaca atttgattcc tttccagcat aacgtcatgt tggttgcaaa 60
aagaaggcaa agtagagcaa gcaagcaagc aaagcatttt tcttatttta tattttgttg 120
cggattccac caccacttg aaaaattgac atgtcacaat gatttcgtat cctagtcttt 180
30 tattatttaa caqtctcaca atcccattac tctacacctc tttcattaag tcaacacacg 240
gttttcaaaa atccactacc ctcccaccac ctagaatctt ttgttaccta ccaacaccct 300
35 cctttgttct ctttatatat tgggtccaact aaatcaataa gggaaagcat ccttttggtt 360
ggaggaattg ctttcattct cactctttgt gtgttgatca atggactagc taataacaag 420
ttcctcctct atatatttca aaagaatgga acagaaacat aaacgaaaga cagagtacct 480
40 gatgttgatg attcattgtc tgtctggagc tcccaaagtc cttttatgct tacatattca 540
taaccaacaa cggctattaa ttataaacca aaaacacgaa ataagtttgt agcaaagtga 600
45 aattaggaat cttggagatg gatccattag tagtaggata ataggatatg atggaatttg 660

5 gttggggaac agtgataact tacgcttgct tccggcgccg ggaaagttgg aaaacctaca 720
 aagtacagaa atggatctgg gccttgaagt gggcttttta ttaaagaaaa aaatacatct 780
 ccgttatcaa tcaccatctt cttctatcta caaattaaag aaggtaacaa cagaacgtgg 840
 tggatcatgt ggtaggcat taattatttg ctttgtttcg ccgttttggt aacacacaga 900
 10 cacagttccg gtaagagctt ttgcagccac tctttatagt tatttagaat tggcgatcga 960
 atcaatctca ctccctccct cccttaagtc ttgttgaatc tgctgaattg ttttataaag 1020
 agttactttg gca 1033
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 20 <212> DNA
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 30 <222>" (1) .. (18)
 <223>
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 atggaagctc ttctcaag 18
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<222> (1)..(18)

<223>

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<400> 170

accttaccta aaacattt ,

18

20

<210> 171

<211> 1666

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<212> DNA

<213> Lycopersicon esculentum

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<220>

<221> CDS

35

<222> (1)..(1494)

<223>

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<400> 171

atg gaa gct ctt ctc aag cct ttt cca tct ctt tta ctt tcc tct cct
Met Glu Ala Leu Leu Lys Pro Phe Pro Ser Leu Leu Leu Ser Ser Pro

48

1

5

10

15

45

266

	aca ccc cat agg tct att ttc caa caa aat ccc tct ttt cta agt ccc	96
	Thr Pro His Arg Ser Ile Phe Gln Gln Asn Pro Ser Phe Leu Ser Pro	
	20 25 30	
5	acc acc aaa aaa aaa tca aga aaa tgt ctt ctt aga aac aaa agt agt	144
	Thr Thr Lys Lys Lys Ser Arg Lys Cys Leu Leu Arg Asn Lys Ser Ser	
	35 40 45	
10	aaa ctt ttt tgt agc ttt ctt gat tta gca ccc aca tca aag cca gag	192
	Lys Leu Phe Cys Ser Phe Leu Asp Leu Ala Pro Thr Ser Lys Pro Glu	
	50 55 60	
15	tct tta gat gtt aac atc tca tgg gtt gat cct aat tgc aat cgg gct	240
	Ser Leu Asp Val Asn Ile Ser Trp Val Asp Pro Asn Ser Asn Arg Ala	
	65 70 75 80	
20	caa ttc gac gtg atc att atc gga gct ggc cct gct ggg ctc agg cta	288
	Gln Phe Asp Val Ile Ile Ile Gly Ala Gly Pro Ala Gly Leu Arg Leu	
	85 90 95	
25	gct gaa caa gtt tct aaa tat ggt att aag gta tgt tgt gtt gac cct	336
	Ala Glu Gln Val Ser Lys Tyr Gly Ile Lys Val Cys Cys Val Asp Pro	
	100 105 110	
30	tca cca ctc tcc atg tgg cca aat aat tat ggt gtt tgg gtt gat gag	384
	Ser Pro Leu Ser Met Trp Pro Asn Asn Tyr Gly Val Trp Val Asp Glu	
	115 120 125	
35	ttt gag aat tta gga ctg gaa aat tgt tta gat cat aaa tgg cct atg	432
	Phe Glu Asn Leu Gly Leu Glu Asn Cys Leu Asp His Lys Trp Pro Met	
	130 135 140	
40	act tgt gtg cat ata aat gat aac aaa act aag tat ttg gga aga cca	480
	Thr Cys Val His Ile Asn Asp Asn Lys Thr Lys Tyr Leu Gly Arg Pro	
	145 150 155 160	
45	tat ggt aga gtt agt aga aag aag ctg aag ttg aaa ttg ttg aat agt	528
	Tyr Gly Arg Val Ser Arg Lys Lys Leu Lys Leu Lys Leu Leu Asn Ser	
	165 170 175	
50	tgt gtt gag aac aga gtg aag ttt tat aaa gct aag gtt tgg aaa gtg	576
	Cys Val Glu Asn Arg Val Lys Phe Tyr Lys Ala Lys Val Trp Lys Val	
	180 185 190	
55	gaa cat gaa gaa ttt gag tct tca att gtt tgt gat gat ggt aag aag	624

267

	Glu	His	Glu	Glu	Phe	Glu	Ser	Ser	Ile	Val	Cys	Asp	Asp	Gly	Lys	Lys	
			195					200					205				
	ata	aga	ggt	agt	ttg	gtt	gtg	gat	gca	agt	ggt	ttt	gct	agt	gat	ttt	672
5	Ile	Arg	Gly	Ser	Leu	Val	Val	Asp	Ala	Ser	Gly	Phe	Ala	Ser	Asp	Phe	
			210				215					220					
	ata	gag	tat	gac	agg	cca	aga	aac	cat	ggt	tat	caa	att	gct	cat	ggg	720
10	Ile	Glu	Tyr	Asp	Arg	Pro	Arg	Asn	His	Gly	Tyr	Gln	Ile	Ala	His	Gly	
			225				230				235					240	
	gtt	tta	gta	gaa	gtt	gat	aat	cat	cca	ttt	gat	ttg	gat	aaa	atg	gtg	768
	Val	Leu	Val	Glu	Val	Asp	Asn	His	Pro	Phe	Asp	Leu	Asp	Lys	Met	Val	
					245					250					255		
15	ctt	atg	gat	tgg	agg	gat	tct	cat	ttg	ggt	aat	gag	cca	tat	tta	agg	816
	Leu	Met	Asp	Trp	Arg	Asp	Ser	His	Leu	Gly	Asn	Glu	Pro	Tyr	Leu	Arg	
				260					265				270				
20	gtg	aat	aat	gct	aaa	gaa	cca	aca	ttc	ttg	tat	gca	atg	cca	ttt	gat	864
	Val	Asn	Asn	Ala	Lys	Glu	Pro	Thr	Phe	Leu	Tyr	Ala	Met	Pro	Phe	Asp	
				275				280					285				
	aga	gat	ttg	gtt	ttc	ttg	gaa	gag	act	tct	ttg	gtg	agt	cgt	cct	gtt	912
25	Arg	Asp	Leu	Val	Phe	Leu	Glu	Glu	Thr	Ser	Leu	Val	Ser	Arg	Pro	Val	
			290				295					300					
	tta	tcg	tat	atg	gaa	gta	aaa	aga	agg	atg	gtg	gca	aga	tta	agg	cat	960
	Leu	Ser	Tyr	Met	Glu	Val	Lys	Arg	Arg	Met	Val	Ala	Arg	Leu	Arg	His	
30			305				310					315				320	
	ttg	ggg	atc	aaa	gtg	aaa	agt	gtt	att	gag	gaa	gag	aaa	tgt	gtg	atc	1008
	Leu	Gly	Ile	Lys	Val	Lys	Ser	Val	Ile	Glu	Glu	Glu	Lys	Cys	Val	Ile	
					325					330				335			
35	cct	atg	gga	gga	cca	ctt	ccg	cgg	att	cct	caa	aat	gtt	atg	gct	att	1056
	Pro	Met	Gly	Gly	Pro	Leu	Pro	Arg	Ile	Pro	Gln	Asn	Val	Met	Ala	Ile	
					340				345				350				
40	ggt	ggg	aat	tca	ggg	ata	gtt	cat	cca	tca	aca	ggg	tac	atg	gtg	gct	1104
	Gly	Gly	Asn	Ser	Gly	Ile	Val	His	Pro	Ser	Thr	Gly	Tyr	Met	Val	Ala	
			355					360				365					
	agg	agc	atg	gct	tta	gca	cca	gta	cta	gct	gaa	gcc	atc	gtc	gag	ggg	1152
45	Arg	Ser	Met	Ala	Leu	Ala	Pro	Val	Leu	Ala	Glu	Ala	Ile	Val	Glu	Gly	

268

	370	375	380	
	ctt ggc tca aca aga atg ata aga ggg tct caa ctt tac cat aga gtt	1200		
	Leu Gly Ser Thr Arg Met Ile Arg Gly Ser Gln Leu Tyr His Arg Val			
5	385	390	395	400
	tgg aat ggt ttg tgg cct ttg gat aga aga tgt gtt aga gaa tgt tat	1248		
	Trp Asn Gly Leu Trp Pro Leu Asp Arg Arg Cys Val Arg Glu Cys Tyr			
	405	410	415	
10	tca ttt ggg atg gag aca ttg ttg aag ctt gat ttg aaa ggg act agg	1296		
	Ser Phe Gly Met Glu Thr Leu Leu Lys Leu Asp Leu Lys Gly Thr Arg			
	420	425	430	
15	aga ttg ttt gac gct ttc ttt gat ctt gat cct aaa tac tgg caa ggg	1344		
	Arg Leu Phe Asp Ala Phe Phe Asp Leu Asp Pro Lys Tyr Trp Gln Gly			
	435	440	445	
20	ttc ctt tct tca aga ttg tct gtc aaa gaa ctt ggt tta ctc agc ttg	1392		
	Phe Leu Ser Ser Arg Leu Ser Val Lys Glu Leu Gly Leu Leu Ser Leu			
	450	455	460	
25	tgt ctt ttc gga cat ggc tca aac atg act agg ttg gat att gtt aca	1440		
	Cys Leu Phe Gly His Gly Ser Asn Met Thr Arg Leu Asp Ile Val Thr			
	465	470	475	480
30	aaa tgt cct ctt cct ttg gtt aga ctg att ggc aat cta gca ata gag	1488		
	Lys Cys Pro Leu Pro Leu Val Arg Leu Ile Gly Asn Leu Ala Ile Glu			
	485	490	495	
	agc ctt tgaatgtgaa aagtttgaat cattttcttc attttaattt ctttgattat	1544		
	Ser Leu			
35	tttcatattt tctcaattgc aaaagtgaga taagagctac atactgtcaa caaataaact	1604		
	actattggaa agttaaata tgtgtttggt gtatgttatt ctaatggaat ggattttgta	1664		
40	aa	1666		
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45	<211> 498			

<212> PRT

<213> Lycopersicon esculentum

5

<400> 172

10 Met Glu Ala Leu Leu Lys Pro Phe Pro Ser Leu Leu Leu Ser Ser Pro
1 5 10 15

15 Thr Pro His Arg Ser Ile Phe Gln Gln Asn Pro Ser Phe Leu Ser Pro
20 25 30

Thr Thr Lys Lys Lys Ser Arg Lys Cys Leu Leu Arg Asn Lys Ser Ser
35 40 45

20 Lys Leu Phe Cys Ser Phe Leu Asp Leu Ala Pro Thr Ser Lys Pro Glu
50 55 60

25 Ser Leu Asp Val Asn Ile Ser Trp Val Asp Pro Asn Ser Asn Arg Ala
65 70 75 80

30 Gln Phe Asp Val Ile Ile Ile Gly Ala Gly Pro Ala Gly Leu Arg Leu
85 90 95

35 Ala Glu Gln Val Ser Lys Tyr Gly Ile Lys Val Cys Cys Val Asp Pro
100 105 110

Ser Pro Leu Ser Met Trp Pro Asn Asn Tyr Gly Val Trp Val Asp Glu
115 120 125

40 Phe Glu Asn Leu Gly Leu Glu Asn Cys Leu Asp His Lys Trp Pro Met
130 135 140

45 Thr Cys Val His Ile Asn Asp Asn Lys Thr Lys Tyr Leu Gly Arg Pro

270

	145		150		155		160									
5	Tyr	Gly	Arg	Val	Ser	Arg	Lys	Lys	Leu	Lys	Leu	Lys	Leu	Leu	Asn	Ser
					165				170						175	
10	Cys	Val	Glu	Asn	Arg	Val	Lys	Phe	Tyr	Lys	Ala	Lys	Val	Trp	Lys	Val
				180					185					190		
15	Glu	His	Glu	Glu	Phe	Glu	Ser	Ser	Ile	Val	Cys	Asp	Asp	Gly	Lys	Lys
			195					200					205			
20	Ile	Arg	Gly	Ser	Leu	Val	Val	Asp	Ala	Ser	Gly	Phe	Ala	Ser	Asp	Phe
			210					215				220				
25	Ile	Glu	Tyr	Asp	Arg	Pro	Arg	Asn	His	Gly	Tyr	Gln	Ile	Ala	His	Gly
	225					230				235					240	
30	Val	Leu	Val	Glu	Val	Asp	Asn	His	Pro	Phe	Asp	Leu	Asp	Lys	Met	Val
				245					250					255		
35	Leu	Met	Asp	Trp	Arg	Asp	Ser	His	Leu	Gly	Asn	Glu	Pro	Tyr	Leu	Arg
			260					265						270		
40	Val	Asn	Asn	Ala	Lys	Glu	Pro	Thr	Phe	Leu	Tyr	Ala	Met	Pro	Phe	Asp
		275						280					285			
45	Arg	Asp	Leu	Val	Phe	Leu	Glu	Glu	Thr	Ser	Leu	Val	Ser	Arg	Pro	Val
		290					295					300				
50	Leu	Ser	Tyr	Met	Glu	Val	Lys	Arg	Arg	Met	Val	Ala	Arg	Leu	Arg	His
	305					310				315				320		
55	Leu	Gly	Ile	Lys	Val	Lys	Ser	Val	Ile	Glu	Glu	Glu	Lys	Cys	Val	Ile
				325					330					335		

Pro Met Gly Gly Pro Leu Pro Arg Ile Pro Gln Asn Val Met Ala Ile
 340 345 350
 5
 Gly Gly Asn Ser Gly Ile Val His Pro Ser Thr Gly Tyr Met Val Ala
 355 360 365
 10
 Arg Ser Met Ala Leu Ala Pro Val Leu Ala Glu Ala Ile Val Glu Gly
 370 375 380
 15
 Leu Gly Ser Thr Arg Met Ile Arg Gly Ser Gln Leu Tyr His Arg Val
 385 390 395 400
 20
 Trp Asn Gly Leu Trp Pro Leu Asp Arg Arg Cys Val Arg Glu Cys Tyr
 405 410 415
 Ser Phe Gly Met Glu Thr Leu Leu Lys Leu Asp Leu Lys Gly Thr Arg
 420 425 430
 25
 Arg Leu Phe Asp Ala Phe Phe Asp Leu Asp Pro Lys Tyr Trp Gln Gly
 435 440 445
 30
 Phe Leu Ser Ser Arg Leu Ser Val Lys Glu Leu Gly Leu Leu Ser Leu
 450 455 460
 35
 Cys Leu Phe Gly His Gly Ser Asn Met Thr Arg Leu Asp Ile Val Thr
 465 470 475 480
 40
 Lys Cys Pro Leu Pro Leu Val Arg Leu Ile Gly Asn Leu Ala Ile Glu
 485 490 495
 Ser Leu

45